

GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: October 29, 2005, 02:46:28 ; Search time 175 Seconds  
(without alignments)  
991.971 Million cell updates/sec

Title: US-09-503-387-3  
Perfect score: 1786  
Sequence: 1 MSPSPALFCLGLGRVPA.....KSHGGQDGRQDVHSGGLCS 339

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1786	100.0	339	2 Q9UIF2	Q9uiF2 homo sapien
2	1676	93.8	321	2 Q9HCN7	Q9hcn7 homo sapien
3	1355	75.9	620	2 Q9HCN6	Q9hcn6 homo sapien
4	499	27.9	447	2 Q6FGQ9	Q6fgq9 homo sapien
5	498	27.9	448	1 LIB4_HUMAN	Q8nhj6 homo sapien
6	478	26.8	481	2 Q8MJZ2	Q8mjz2 pan troglod
7	469	26.3	325	1 NCT1_RAT	Q9z0h5 rattus norv
8	464	26.0	631	2 Q8MJZ3	Q8mjz3 pan troglod
9	459	25.7	304	1 NCT1_HUMAN	Q76036 homo sapien
10	455	25.5	325	1 NCT1_MOUSE	Q8c567 mus musculu
11	455	25.5	645	2 Q8MJZ5	Q8mjz5 pan troglod
12	448	25.1	631	1 LIB3_HUMAN	Q75022 homo sapien
13	443.5	24.8	306	2 Q8MIZ8	Q8miz8 macaca mulla
14	443	24.8	307	2 Q8MIZ9	Q8miz9 macaca mulla
15	442.5	24.8	499	1 LIB4_HUMAN	P59901 homo sapien
16	441.5	24.7	460	2 Q8MJZ4	Q8mjz4 pan troglod
17	441	24.7	483	1 LIB2_HUMAN	Q8ni49 homo sapien
18	440.5	24.7	306	1 NCT1_MACFA	Q95jb9 macaca fasc
19	438.5	24.6	489	1 LIB1_HUMAN	Q75019 homo sapien
20	436	24.4	305	2 Q8MIZ7	Q8miz7 macaca mulla
21	435.5	24.4	305	2 Q8MIZ6	Q8miz6 macaca mulla
22	434	24.3	598	1 LIB2_HUMAN	Q8n423 h leukocyte
23	429	24.0	590	1 LIB5_HUMAN	Q75023 homo sapien
24	428	24.0	472	2 Q6PIZ7	Q6piz7 homo sapien
25	426.5	23.9	264	2 Q28109	Q28109 bos taurus
26	424.5	23.8	643	1 LIB5_PANTR	Q8mjz7 pan troglod
27	424.5	23.8	662	2 Q8MJZ6	Q8mjz6 pan troglod
28	422	23.6	336	2 Q8SPQ5	Q8spq5 bos taurus
29	421.5	23.6	650	1 LIB1_HUMAN	Q8nh16 h leukocyte
30	408.5	22.9	439	1 LIB3_HUMAN	Q8n6c8 homo sapien
31	401.5	22.5	294	2 Q8MIZ5	Q8miz5 macaca mulla

32	394	22.1	382	2 Q8NF80	Q8nF80 homo sapien
33	392	21.9	287	1 FCAR_HUMAN	P24071 homo sapien
34	392	21.9	308	1 NCT1_BOVIN	Q863h2 bos taurus
35	372.5	20.9	697	2 Q8K4V6	Q8k4v6 mus musculu
36	372.5	20.9	841	2 Q8R2Z1	Q8r2z1 mus musculu
37	365.5	20.5	635	2 Q55002	Q55002 mus musculu
38	364.5	20.4	369	2 Q8MK12	Q8mk12 macaca mulla
39	363	20.3	193	2 Q6PI73	Q6pi73 homo sapien
40	362.5	20.3	841	2 Q54999	Q54999 mus musculu
41	361.5	20.2	357	2 Q8MK11	Q8mk11 macaca mulla
42	358	20.0	663	2 Q70434	Q70434 mus musculu
43	356.5	20.0	680	2 Q55001	Q55001 mus musculu
44	351	19.7	275	2 Q9UEK0	Q9uek0 homo sapien
45	349.5	19.6	367	2 Q8MK08	Q8mk08 macaca mulla

ALIGNMENTS

RESULT 1				
Q9UIF2				
ID	Q9UIF2	PRELIMINARY;	PRT;	339 AA.
AC	Q9UIF2;			
DT	01-MAY-2000 (Tremblrel. 13, Created)			
DT	01-MAY-2000 (Tremblrel. 13, Last sequence update)			
DT	05-JUL-2004 (Tremblrel. 27, Last annotation update)			
DE	platelet glycoprotein VI precursor (platelet glycoprotein VI-1).			
GN	Name-gpVI; Synonyms-GpVI;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]_TaxID=9606;			
RP	SEQUENCE FROM N.A.			
RA	Mura Y.;			
RL	Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20483673; PubMed=11027634; DOI=10.1006/bbrc.2000.3624;			
RA	Ezumi Y., Uchiyama T., Takayama H.;			
RT	"Molecular cloning, genomic structure, chromosomal localization, and alternative splice forms of the platelet collagen receptor glycoprotein VI.";			
RT	glycoprotein VI.";			
RL	Biochem. Biophys. Res. Commun. 277:27-36(2000).			
DR	EMBL; AB035073; BAA89353.1; --			
DR	EMBL; AB043819; BAB12245.1; --			
DR	PIR; JC7509; JC7509.			
DR	HSSP; Q8NHL6; IG0X.			
DR	GO; GO:0005887; C:integral to plasma membrane; TAS.			
DR	GO; GO:0005518; F:collagen binding; TAS.			
DR	GO; GO:0004888; F:transmembrane receptor activity; TAS.			
DR	GO; GO:0007167; P:enzyme linked receptor protein signaling pa. . .; TAS.			
DR	InterPro; IPR003599; IG.			
DR	InterPro; IPR007110; IG-like.			
DR	InterPro; IPR001847; Peptidase_S21.			
DR	Pfam; PF00047; ig; 1.			
DR	SMART; SM00409; IG; 2.			
KW	Signal.			
FT	SIGNAL	1	20	Potential.
FT	CHAIN	21	339	Potential.
SQ	SEQUENCE	339 AA;	36923 MW;	423756E95E030CC CRC64;

Query Match				
Best Local Similarity 100.0%; Score 1786; DB 2; Length 339;				
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1	MSPSPALFCLGLGRVPAQSGPLPKPSLOALPSSLVPLEKPVTLRCQGGPGVDLYRLE	60	
Db	1	MSPSPALFCLGLGRVPAQSGPLPKPSLOALPSSLVPLEKPVTLRCQGGPGVDLYRLE	60	
QY	61	KLSSRYQDQAVLFIPAMKRSAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQ	120	
Db	61	KLSSRYQDQAVLFIPAMKRSAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQ	120	

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Qy 121 GPAVSSGGDVTLCQCTRYGDFQFALYKEGDPAPYKNPERWYRASFPFIITVTAHSGTYRC 180
Db 121 GPAVSSGGDVTLCQCTRYGDFQFALYKEGDPAPYKNPERWYRASFPFIITVTAHSGTYRC 180

Qy 181 YFSRSRDPLYMSAPSDPLELVVVTGTSVTPSPRLPTEPPSSVAEFSATAELTVSFNKNVFT 240
Db 181 YFSRSRDPLYMSAPSDPLELVVVTGTSVTPSPRLPTEPPSSVAEFSATAELTVSFNKNVFT 240

Qy 241 TETSRITTSKESDSPAGPARQYTYKGNLVRIICLGAVILIILAGFLAEDWHSRRKRLRH 300
Db 241 TETSRITTSKESDSPAGPARQYTYKGNLVRIICLGAVILIILAGFLAEDWHSRRKRLRH 300

Qy 301 RGRAVQRLPLPLPOTRKSHGQDGRQDVHSGRLCS 339
Db 301 RGRAVQRLPLPLPOTRKSHGQDGRQDVHSGRLCS 339

RESULT 2
Q9HCN7 PRELIMINARY; PRT; 321 AA.
ID Q9HCN7 AC Q9HCN7;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Platelet glycoprotein VI-2.
GN Name=GPVI;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20483673; PubMed=11027634; DOI=10.1006/bbrc.2000.3624;
RA Ezumi Y., Uchiyama T., Takayama H.;
RT "Molecular cloning, genomic structure, chromosomal localization, and
RT alternative splice forms of the platelet collagen receptor
RT glycoprotein VI.";
RL Biochem. Biophys. Res. Commun. 277:27-36(2000).
DR EMBL; AB043820; BAB12246.1; -.
DR HSSP; O8NHL6; 1GOX.
DR GO; GO:0004252; P:serine-type endopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00409; IG; 2.
SQ SEQUENCE 321 AA; 35158 MW; 93F8F88945958345 CRC64;

Query Match 93.8%; Score 1676; DB 2; Length 321;
Best Local Similarity 94.7%; Pred. No. 2.6e-115;
Matches 321; Conservative 0; Mismatches 0; Indels 18; Gaps 1;

Qy 1 MSPSPTALFCLGCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRLE 60
Db 1 MSPSPTALFCLGCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRLE 60

Qy 61 KLSRSRYODQAVLFIPAMKRSIAGRYCSYONGSLWSLPSDQLELVATGVFAKPSLSAQ 120
Db 61 KLSRSRYODQAVLFIPAMKRSIAGRYCSYONGSLWSLPSDQLELVATGVFAKPSLSAQ 120

Qy 121 GPAVSSGGDVTLCQCTRYGDFQFALYKEGDPAPYKNPERWYRASFPFIITVTAHSGTYRC 180
Db 121 GPAVSSGGDVTLCQCTRYGDFQFALYKEGDPAPYKNPERWYRASFPFIITVTAHSGTYRC 180

Qy 181 YFSRSRDPLYMSAPSDPLELVVVTGTSVTPSPRLPTEPPSSVAEFSATAELTVSFNKNVFT 240
Db 181 YFSRSRDPLYMSAPSDPLELVVVTGTSVTPSPRLPTEPPSSVAEFSATAELTVSFNKNVFT 240

Qy 241 TETSRITTSKESDSPAGPARQYTYKGNLVRIICLGAVILIILAGFLAEDWHSRRKRLRH 300
Db 241 TETSRITTSKESDSPAGPARQYTYKGNLVRIICLGAVILIILAGFLAEDWHSRRKRLRH 300

Qy 301 RGRAVQRLPLPLPOTRKSHGQDGRQDVHSGRLCS 339
Db 301 RGRAVQRLPLPLPOTRKSHGQDGRQDVHSGRLCS 339
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Qy 301 RGRAVQRLPLPLPOTRKSHGQDGRQDVHSGRLCS 339
Db 283 RGRAVQRLPLPLPOTRKSHGQDGRQDVHSGRLCS 321

RESULT 3
Q9HCN6 PRELIMINARY; PRT; 620 AA.
ID Q9HCN6 AC Q9HCN6;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Platelet glycoprotein VI-3.
GN Name=GPVI;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20483673; PubMed=11027634; DOI=10.1006/bbrc.2000.3624;
RA Ezumi Y., Uchiyama T., Takayama H.;
RT "Molecular cloning, genomic structure, chromosomal localization, and
RT alternative splice forms of the platelet collagen receptor
RT glycoprotein VI.";
RL Biochem. Biophys. Res. Commun. 277:27-36(2000).
DR EMBL; AB043821; BAB12247.1; -.
DR HSSP; O8NHL6; 1GOX.
DR GO; GO:0016021; C:integral to membrane; NAS.
DR GO; GO:0005518; F:collagen binding; TAS.
DR GO; GO:0004812; F:receptor activity; TAS.
DR GO; GO:0030168; P:platelet activation; NAS.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR001847; Peptidase_S21.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00409; IG; 2.
SQ SEQUENCE 620 AA; 67308 MW; FBEE64C55F679615 CRC64;

Query Match 75.9%; Score 1355; DB 2; Length 620;
Best Local Similarity 100.0%; Pred. No. 2.4e-91;
Matches 259; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSPSPTALFCLGCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRLE 60
Db 1 MSPSPTALFCLGCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRLE 60

Qy 61 KLSRSRYODQAVLFIPAMKRSIAGRYCSYONGSLWSLPSDQLELVATGVFAKPSLSAQ 120
Db 61 KLSRSRYODQAVLFIPAMKRSIAGRYCSYONGSLWSLPSDQLELVATGVFAKPSLSAQ 120

Qy 121 GPAVSSGGDVTLCQCTRYGDFQFALYKEGDPAPYKNPERWYRASFPFIITVTAHSGTYRC 180
Db 121 GPAVSSGGDVTLCQCTRYGDFQFALYKEGDPAPYKNPERWYRASFPFIITVTAHSGTYRC 180

Qy 181 YFSRSRDPLYMSAPSDPLELVVVTGTSVTPSPRLPTEPPSSVAEFSATAELTVSFNKNVFT 240
Db 181 YFSRSRDPLYMSAPSDPLELVVVTGTSVTPSPRLPTEPPSSVAEFSATAELTVSFNKNVFT 240

Qy 241 TETSRITTSKESDSPAG 259
Db 241 TETSRITTSKESDSPAG 259

RESULT 4
Q9FGQ9 PRELIMINARY; PRT; 447 AA.
ID Q9FGQ9 AC Q9FGQ9;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
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CC -!- SUBUNIT: Binds PTPN6 when phosphorylated.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Ligand binding
CC leads to internalization and translocation to an antigen-
CC processing compartment.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q8NHJ6-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q8NHJ6-2; Sequence=VSP_008460;
CC Note=Alternative use of an acceptor site. No experimental
CC confirmation available;
CC -!- TISSUE SPECIFICITY: Detected in monocytes, macrophages, dendritic
CC cells, lung, natural killer cells and B-cells.
CC -!- INDUCTION: Upon contact with CD8(+)CD28(-) alloantigen-specific T
CC suppressor (Ts) cells.
CC -!- DOMAIN: Contains 3 copies of a cytoplasmic motif that is referred
CC to as the immunoreceptor tyrosine-based inhibitor motif (ITIM).
CC This motif is involved in modulation of cellular responses. The
CC phosphorylated ITIM motif can bind the SH2 domain of several SH2-
CC containing phosphatases.
CC -!- PTM: Phosphorylated.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U91925; AAB6665.1; -.
DR EMBL; AF025532; AAB87666.1; -.
DR EMBL; AF189768; AAG02024.1; -.
DR EMBL; AF283988; AAL3692.1; -.
DR EMBL; BC026309; AAH26309.1; -.
DR HSSP; Q8NHL6; IGOX.
DR Genew; HGNC:6608; LILRB4.
DR H-InvdB; HIX0020913; -.
DR MIM; 604821; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; Ig; 1.
DR PROSITE; PS0835; IG LIKE; 2.
KW Alternative splicing; Antigen; Immune response; Immunoglobulin domain;
KW Multigene family; Phosphorylation; Polymorphism; Receptor; Repeat;
KW Signal; Transmembrane.
FT SIGNAL 1 21
FT CHAIN 22 448
FT DOMAIN 22 259
FT TRANSMEM 260 280
FT DOMAIN 281 448
FT DOMAIN 27 118
FT DOMAIN 124 218
FT DISULFID 49 98
FT DISULFID 144 195
FT SITE 358 363
FT SITE 410 415
FT SITE 440 445
FT VARSPLIC 348 348
FT VARIANT 223 223
FT VARIANT 362 362
FT VARIANT 5 5
FT CONFLICT 20 20
FT CONFLICT 414 414
FT CONFLICT 414 414
SQ SEQUENCE 448 AA; 49297 MW; 76D1E24A82EA1399 CRC64;
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Query Match 27.9%; Score 498; DB 1; Length 448;
Best Local Similarity 36.0%; Pred. No. 1.9e-28;
Matches 133; Conservative 41; Mismatches 127; Indels 68; Gaps 9;

QY 1 MSPSPALFCLGLCLG-RVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPVGVLYRL 59
DB 1 MIPTTALLCLGLSLGRTHMQAGPLPKPTLWAEFGSVISWGNSTVTWCQGTLEAREYRL 60

QY 60 EKLSSRYQD-----QAVLFIPAMKRSAGRYCSYQNGSLWSLPDQLBELVATGV 110
DB 61 DKESPAPMDQRNPLEPKNKARFSPSTEDYAGRYCYRSPVGVWSQSPDLELVMTGA 120

QY 111 FAKSLSAQPCPAYSAGDVTLCOTRYGDFQFALYKEGPAPY-----KNPERWYRAS 165
DB 121 YSKPTLSALPSPLVTSGKSVTLCCQSRPMDTFLLIKERAAPHLHLRSEHGAQOHOAE 180

QY 166 PIITVTAHSQTYRCYCSFSSRDPLYMSAPSDPLELVLTGTSTVPSRLPTEPSSVAE 225
DB 181 PMSPTSVHGTYRCFSHGFHYLLSHPSDPLELVSGSLGEGRPSPPT----- 229

QY 226 ATAEITVSTNKNVFTTSTTSITTSKPESQSPAGPARQYITKG-----NLVRIC 279
DB 230 -----RSVTAAGPEDQLMPTGTVSPHSGLRHHEVLIGLVLSIL 270

QY 280 LIILAGP-LAEDWHSRRKR-LRHGRAVORPLPLPLPOTRKSHGGDQGRQ----- 330
DB 271 LLSLLFLLLQHWROGKHRTLAQADQFQRPGAEP-----KDGGLQRRSPAA 322

QY 331 DVHSRGLCS 339
DB 323 DVQENFCA 331

RESULT 6
Q8MJ22 PRELIMINARY; PRT; 481 AA.
AC Q8MJ22
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Leukocyte immunoglobulin-like receptor e.
GN Name=LiRe;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21555186; PubMed=11698452;
RA Canavez F.C., Young N.T., Guethlein L.A., Rajalingam R., Khakoo S.I.,
RA Shum B.P., Parham P.;
RT "Comparison of chimpanzee and human leukocyte Ig-like receptor genes
RT reveals framework and rapidly evolving genes.";
RL J. Immunol. 167:5786-5794(2001).
DR EMBL; AF383169; AAL31878.1; -.
DR HSSP; Q8NHL6; IGOX.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
SQ SEQUENCE 481 AA; 52438 MW; 3FBFC7E8724BF0FC CRC64;
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Query Match 26.8%; Score 478; DB 2; Length 481;
Best Local Similarity 26.6%; Pred. No. 6e-27;
Matches 136; Conservative 41; Mismatches 80; Indels 254; Gaps 9;

QY 1 MSPSPALFCLGLCLG-RVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPVGVLYRL 59
DB 1 MTPALTALLCLGLSLGRTHVQAGPLPKPTLWAEFGSVISWRSPTVTCQGSLEAQAQYRL 60
```



QY 60 EKLSRRYQD-----QAVLFTPAMKRSIAGRYCSYQNGSLWSLPSDQLELVATGV 110  
 DB 61 YKGSREPRDTONPMPKRNKARFSPMTEHAGRYCYRSPAGWSEPSDPLELVVTF 120  
 QY 111 FAKPSLSAQPGPAVSSGGDVTLCQCTRYCFDQFALYKEG----- 149  
 DB 121 YSTPLSALPSPVAVSGGNVTLRCGSKQGYDHFVLMKEGHEQLPOTLDSQHLHSGFQAL 180  
 QY 150 -----DP-----AP----- 153  
 DB 181 FVGVPTPSHRTFTCYGRYNTPTQVMSHPSPLEILPFGVSRKPSLLTLQGPVLAPGES 240  
 QY 154 -----YKNPER----- 159  
 DB 241 LTLQCGSDVGYDRFTLYKEGERDFLQPCQPQAGLSQANFTLPGVSRSHGQYRCYGAH 300  
 QY 160 -----W----- 160  
 DB 301 NLSSEMSAPSDPLNILLIAGQFYDRVSLSLQDPPTVASGENVTLQCQSQQDFTLFLTKEG 360  
 QY 161 -----YRASFPITVTAAHSGTYRCYCFSSRDPVLMWAPSDDPLELVTF 204  
 DB 361 AAHPPLRLRSKYQSKYQAEFFPMNPVTSAAHAGTYRCYGSYSSNPHELLSPSPDLKLMVSG 420  
 QY 205 TSVTSRLPTEPSPSSVABSEATAELTVSFTKNVFTTTSRITTSRKESDSDPAGPARQY 264  
 DB 421 PSGGSLPPTGPPS-----TPASHAKD- 442  
 QY 265 YTKGNLVRICLGAVALIILLAGFLAEDWHSRR 295  
 DB 443 YTVENLIRMGAGLVVLVGLLFEAQHSQR 473

## RESULT 7

NC11 RAT  
 ID NCT1 RAT STANDARD; PRT; 325 AA.  
 AC Q9Z0H5;  
 DT 05-JUL-2004 (Rel. 44, Created)  
 DT 05-JUL-2004 (Rel. 44, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Natural cytotoxicity triggering receptor 1 precursor (Natural killer cell p46-related protein) (NKP46) (Rat activating receptor 1) (rAR-1) (Lymphocyte antigen 94 homolog) (NK receptor KILR-1) (NKATR).  
 GN Name=Ncr1; Synonyms=Arl, Klr1, Ly94;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.  
 RC TISSUE=Lymphoid;  
 RX PubMed=10424451; DOI=10.1016/S0165-2478(99)00052-8;  
 RA Falco M., Cantoni C., Bottino C., Moretta A., Biassoni R.;  
 RT "Identification of the rat homologue of the human Nkp46 triggering receptor.";  
 RL Immunol. Lett. 68:411-414 (1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PVG;  
 RA Berg S.F., Dissen E., Westgaard I.H., Fossum S.;  
 RT "Molecular characterization of KILR-1, a novel immunoglobulin-like gene in the rat, expressed by NK cells.";  
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Cytotoxicity activating receptor that may contribute to the increased efficiency of activated natural killer (NK) cells to mediate tumor cell lysis (By similarity).  
 CC -!- SUBUNIT: Interacts with CD3z and FCER1G (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
 CC -!- TISSUE SPECIFICITY: Weakly expressed in spleen, heart and lung.  
 CC -!- SIMILARITY: Belongs to the natural cytotoxicity receptor (NCR) family.  
 CC -!- SIMILARITY: Contains 2 immunoglobulin-like domains.

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 CC -----

DR EMBL; AJ012741; CAA10161.1; --  
 DR EMBL; AF082533; AAC69890.1; --  
 DR HSSP; Q8NHL6; IG0X.  
 DR RGD; 621288; Ly94.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003599; IG.  
 DR Pfam; PF00047; Ig; 2.  
 DR SMART; SM00409; Ig; 2.  
 DR PROSITE; PS50835; IG LIKE; FALSE NEG.  
 KW Glycoprotein; Immunoglobulin domain; Receptor; Repeat; Signal;  
 KW Transmembrane.  
 FT SIGNAL 1 16 Potential.  
 FT CHAIN 17 325 Natural cytotoxicity triggering receptor 1.  
 FT DOMAIN 17 258 Extracellular (Potential).  
 FT TRANSMEM 259 279 Potential.  
 FT DOMAIN 280 325 Cytoplasmic (Potential).  
 FT DOMAIN 42 100 Ig-like 1.  
 FT DOMAIN 137 192 Ig-like 2.  
 FT DISULFID 49 98 Potential.  
 FT DISULFID 144 190 By similarity.  
 FT CARBOHYD 139 139 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 216 216 N-linked (GlcNAc...) (Potential).  
 SQ SEQUENCE 325 AA; 37178 MW; 502C10AA02F65FA4 CRC64;

Query Match 26.3%; Score 469; DB 1; Length 325;

Best Local Similarity 37.7%; Pred. No. 1.7e-26;  
 Matches 116; Conservative 38; Mismatches 116; Indels 38; Gaps 5;

QY 1 MSPSPALFCLGLCLG-RVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGGVDLYR- 58  
 DB 1 MLPTTALCLGLCLGSLQRINTEKQLPRPIWAKSINWTKGNSVNWICQQAASEYQL 60  
 QY 59 -----LEKLSRRYQDQAVLFTPAMKRSIAGRYCSYQNGSLWSLPSDQLELVATGV 110  
 DB 61 YPEGFFALERPKSRSMNVKFFISQMTSHTAGIYTCFYQSGELWSESNPLKLVVTGL 120  
 QY 111 FAKPSLSAQPGPAVSSGGDVTLCQCTRYCFDQFALYKEGDPAPYKNPERWYASPEITV 170  
 DB 121 YDTPTLWVHPGPEVTLGENVTFSCHLKTATSKFLLKERESNHIQHKYGNIOAEFPMGPV 180  
 QY 171 TAAHSGTYRCYSFSSRDPVLMWAPSDDPLELVVTFSTVTPSRLETPPPSVA--EFSEATA 228  
 DB 181 TAAHSGTYRC--FGSYNDYAMSPPEVTLITGEVNTSLAPTDPVSSLDYWEFDLS- 237  
 QY 229 ELTVSFTKNVFTTTSRITTSRKESDSDPAGPARQYTKGNLVRICLGAVALIILLAGFLA 288  
 DB 238 -----KESGLQKDSAFWDHTAQLIRIGLACIIIVMALVWLLA 274  
 QY 289 EDWHSRRK 296  
 DB 275 EDWLSRRK 282

## RESULT 8

Q8MJZ3  
 ID Q8MJZ3 PRELIMINARY; PRT; 631 AA.  
 AC Q8MJZ3;  
 DT 01-OCT-2002 (TRENBLrel. 22, Created)  
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)  
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
 DE Leukocyte immunoglobulin-like receptor d.  
 GN Name=LIRd;  
 OS Pan troglodytes (Chimpanzee).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;



CC IsoId=O76036-5; Sequence=VSP\_010406;  
 CC Note=No experimental confirmation available;  
 CC -!- TISSUE SPECIFICITY: Selectively expressed by both resting and  
 CC activated NK cells.

CC -!- SIMILARITY: Belongs to the natural cytotoxicity receptor (NCR)  
 CC family.

CC -!- SIMILARITY: Contains 2 immunoglobulin-like domains.

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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----  
 CC EMBL; AJ006121; CAA06872.1; -  
 CC EMBL; AJ006122; CAA06873.1; -  
 CC EMBL; AJ006123; CAA06874.1; -  
 CC EMBL; AJ001383; CAA04714.1; -  
 CC EMBL; AY346373; AAQ54328.1; -  
 CC EMBL; BC064806; AAH64806.1; -  
 CC PDB; 1OL1; X-ray; A=-  
 CC PDB; 1P6F; X-ray; A=22-263.  
 CC Genew; HGNC:6731; NCBI.

CC MIM; 604530; -  
 CC GO; GO:0005887; C:integral to plasma membrane; TAS.  
 CC GO; GO:0005057; F:receptor signaling protein activity; TAS.  
 CC GO; GO:0006968; P:cellular defense response; TAS.  
 CC GO; GO:0007165; P:signal transduction; TAS.

CC InterPro; IPR003599; IG.  
 CC InterPro; IPR007110; IG-like.

CC Pfam; PF00047; ig; 1.  
 CC SMART; SM00409; IG; 1.

CC PROSITE; PS00835; IG LIKE; FALSE NEG.

CC 3D-structure; Alternative splicing; Glycoprotein;

CC Immunoglobulin domain; Polymorphism; Receptor; Repeat; Signal;

CC Transmembrane.

FT SIGNAL 1 21 Potential.

FT CHAIN 22 304 Natural cytotoxicity triggering receptor

FT DOMAIN 22 258 Extracellular (Potential).

FT TRANSMEM 259 279 Potential.

FT DOMAIN 280 304 Cytoplasmic (Potential).

FT DOMAIN 34 118 IG-like 1.

FT DOMAIN 129 211 IG-like 2.

FT DISULFID 49 98

FT DISULFID 144 190

FT CARBOHYD 125 125

FT CARBOHYD 216 216

FT CARBOHYD 225 225

FT VARSPLIC 12 118

FT VARSPLIC 25 119

FT VARSPLIC 228 244

FT VARSPLIC 82 82

FT VARSPLIC 228 228

FT VARSPLIC 304 AA; 34480 MW; PBCBDE50D2F34CD3 CRC64;

FT VARSPLIC 25.7%; Score 459; DB 1; Length 304;

FT VARSPLIC 36.1%; Pred. No. 8.6e-26;

FT VARSPLIC 45; Mismatches 108; Indels 54; Gaps 9;

FT VARSPLIC 1 MSBSPALFCGLICG-RVPAQSGPLPKSLQALPSLSVLEKPTVLRCCGPGVDLYEL 59

FT VARSPLIC 1 MSSTLPALLCVGLICRISAQQTLPKPFIWAEPHFVMPKEKQVTCGNGVAYEYOL 60

FT VARSPLIC 60 -----EKLSSRYDQAVLFIIPAKESLAGRYRCSYONGSLMSLPDQLE 104

FT VARSPLIC 61 HFEGLFAVDRPKPPRINKVPE-----YIPDNRMAGQYSCIYRVGLWSEPNLLD 114

FT VARSPLIC Query Match

FT VARSPLIC Best Local Similarity

FT VARSPLIC Matches 117; Conservative

FT VARSPLIC

FT VARSPLIC

FT VARSPLIC

FT VARSPLIC

FT VARSPLIC

FT VARSPLIC

FT VARSPLIC

FT VARSPLIC

FT VARSPLIC

FT VARSPLIC

FT VARSPLIC

FT VARSPLIC

FT VARSPLIC

QY 105 LVATGVFAKPSLSAQRGPVAVSSGGDVTLLQCOTRYGDFQFALYKEGDPAPYKNPERWYRAS 164  
 DB 115 LVVTEMDDPTLSVHPGPEVIGSEKVTYFCRLDTATSMFLLLKEGRSHVQGYKGVQAE 174  
 QY 165 FPIITVTAHSGTYRCYCSFSSRDPYLSAPSDPLELVVTG-----TSVTPSLRPTPPSSV 220  
 DB 175 FPLGPVTTAHRGTYRC--FGSYNNHAWSPFSEPVKLLVTGDIENSTSLAPED-PTFPADTW 231  
 QY 221 APESEATRLVSTNKNVFTTETSRSTTSKESDSPAGPARQYVTKGNLVICIGAVIL 280  
 DB 232 GTY-----LLTTETG-----LQDKH-----ALMDHTAQNLLRMGLAFLVL 266  
 QY 281 ILAGFLAEDWHSRRKRLRHGRGA 304  
 DB 267 VALVWFLVEDWLSRKTRERASRA 290

# RESULT 10

## NCT1 MOUSE

ID NCT1 MOUSE STANDARD; PRT; 325 AA.

AC Q8C567; Q8OUY6; Q9Z0Q4;

DT 05-JUL-2004 (Rel. 44, Created)

DT 05-JUL-2004 (Rel. 44, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Natural cytotoxicity triggering receptor 1 precursor (Natural killer

cell p46-related protein) (NKP46) (mNKP46) (NK-p46) (Mouse activating

receptor 1) (MAR-1) (Lymphocyte antigen 94).

DE Name=Ncr1; Synonyms=Ly94;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.

RC TISSUE=Lymphoid;

RX MEDLINE=99190527; PubMed=10092106;

RX DOI=10.1002/(SICI)1521-4141(199903)29:03<1014::AID-IMMU1014>3.0.CO;2-O;

RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojibori T.,

RA Baladrelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,

RA Blake J.A., Bradt D., Brusci V., Chothia C., Corbani L.E., Cousins S.,

RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,

RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RA Grummond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,

RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

RA Kongaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

RA Nagashima T., Numata K., Okido T., Pavan W.J., Perce G., Pesole G.,

RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,

RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,

RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita K.,

RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,

RA Wu Y., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,

RA Yuan Z., Zavanian M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,

RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,

RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,

RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,

RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,

RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,

RA Birney E., Hayashizaki Y.;

RA "Analysis of the mouse transcriptome based on functional annotation of

RT 60,770 full-length cDNAs. ;  
RL Nature 420:563-573 (2002).  
RN [3]  
RP SEQUENCE OF 3-325 FROM N.A.  
RC STRAIN=FVB/N; TISSUE=Breast tumor; DOI=10.1073/pnas.242603899;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusik A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences".  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
CC -!- FUNCTION: Cytotoxicity activating receptor that may contribute to  
the increased efficiency of activated natural killer (NK) cells to  
mediate tumor cell lysis (By similarity).  
CC -!- SUBUNIT: Interacts with CD3Z and FCER1G (By similarity).  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
CC -!- TISSUE SPECIFICITY: Selectively expressed by NK cells.  
CC -!- SIMILARITY: Belongs to the natural cytotoxicity receptor (NCR)  
family.  
CC -!- SIMILARITY: Contains 2 immunoglobulin-like domains.  
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DR EMBL; AJ223765; CAB39169.1; -;  
DR EMBL; AK079401; BAC37635.1; -;  
DR EMBL; BC042788; AAH42788.1; -;  
DR HSP; Q8NHL6; IG0X.  
DR MGP; MGI:1336212; Nr1.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00409; IG; 2.  
DR PROSITE; PS00835; IG LIKE; FALSE NEG.  
KW Glycoprotein; Immunoglobulin domain; Receptor; Repeat; Signal;  
KW Transmembrane.  
FT SIGNAL 1 16 Potential.  
FT CHAIN 17 325 Natural cytotoxicity triggering receptor  
FT FT 1.  
FT DOMAIN 17 255 Extracellular (Potential).  
FT TRANSMEM 256 273 Potential.  
FT DOMAIN 274 325 Cytoplasmic (Potential).  
FT DOMAIN 34 118 Ig-like 1.  
FT DOMAIN 129 211 Ig-like 2.  
FT DISULFID 49 98 Potential.  
FT DISULFID 144 190 Potential.  
FT CARBOHYD 139 139 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 216 216 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 238 238 N-linked (GlcNAc...) (Potential).  
FT CONFLICT 131 131 R -> Q (in Ref. 2).  
SQ SEQUENCE 325 AA; 37265 MW; ED24E48BF22F029 CRC64;

Query Match

25.5%; Score 455; DB 1; Length 325;

Best Local Similarity 38.0%; Pred. No. 1.8e-25;  
Matches 117; Conservative 36; Mismatches 117; Indels 38; Gaps 6;  
QY 1 MSPSPTALFCLGCLG-RVPAQSGPLPKPSLOALPSSLVPLEKPVTLRCQGPVGVLYR- 58  
DB 1 MLPTLTALLCLGCLCRLQINTEKTPKPIWAKPSIWMVINGNSVNIWCQAQASAYQL 60  
QY 59 -----LEKLSRRYQDQAVLFIKPKSLAGRYCSYONGSLWSLPSDLELVATGV 110  
DB 61 YFEGSFFALERPSPKSRMKNKVRFFISQMTSHTAGIYTCFYQSGELMSKSNPLKLVVGL 120  
QY 111 FAKPSLSAQPGPAVSSGGDVTLOQTRYGDFQFALYKEGDPAPYKNPWRWRASFPFIITV 170  
DB 121 YDTNLWVYPRPEVTGLNVTFFCQLKTATSKFLLKXGNSHNIQNKYGNIOAFPMGPV 180  
QY 171 TAAHSGTYRCYFSFSDPYLWMSAPDLELVVTGTVTPSLPTEPPSSVA--BFSEATA 228  
DB 181 TRAHRTYRC--FGSYNDYAWSPFSEPTLLITGVENSSSLAPDPTSSLDYWFEDLSTN 238  
QY 229 ELTVSFTNKVFTTSRISITSPKESDPAGPAQYTKGNLVRICLGAVALIILAGELA 288  
DB 239 E-----SGLOKDS---AFWDHTTQNLIRIGLACIILITLVMLLT 274  
QY 289 EDWHSRRK 296  
DB 275 EDWLSRRK 282  
ID Q8MJZ5 PRELIMINARY; PRT; 645 AA.  
AC Q8MJZ5;  
DT 01-OCT-2002 (TREMblrel. 22, Created)  
DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)  
DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)  
DE Leukocyte immunoglobulin-like receptor b.  
GN Name=LiRb;  
OS Pan troglodytes (Chimpanzee).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
ON NCBI\_TaxID=9598;  
RX SEQUENCE FROM N.A.  
RP MEDLINE=21555186; PubMed=11698452;  
RA Canavez F.C., Young N.T., Guethlein L.A., Rajalingam R., Khakoo S.I.,  
RA Shum B.P., Parham P.;  
RT "Comparison of chimpanzee and human leukocyte Ig-like receptor genes  
reveals framework and rapidly evolving genes.";  
RL J. Immunol. 167:5786-5794(2001).  
DR EMBL; AF383166; AAL31875.1; -;  
DR HSP; Q8NHL6; IG0X.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00409; IG; 3.  
DR PROSITE; PS00835; IG LIKE; 2.  
KW Receptor.  
SQ SEQUENCE 645 AA; 69898 MW; A032ED6BDE8FB144 CRC64;  
Query Match 25.5%; Score 455; DB 2; Length 645;  
Best Local Similarity 39.8%; Pred. No. 4.2e-25;  
Matches 121; Conservative 36; Mismatches 115; Indels 32; Gaps 10;  
QY 1 MSPSPTALFCLGCLG-RVPAQSGPLPKPSLOALPSSLVPLEKPVTLRCQGPVGVLYR- 56  
DB 1 MTPILTTLVLCGLSLGPRTHVQAGTLPKPTLRAPSDSVITQGSPTVTLRCQGSLEAQNHL 60  
QY 57 YRLKLS--SRYQDAV-----LFIKPKSLAGRYCSYONGSLWSLPSDLELVATGV 110  
DB 61 YREKKSASWIKRIQPLVKKGQFPFIPSTWEGRYRCQYYSRQWSFSDPPELVVTA 120  
QY 111 FAKPSLSAQPGPAVSSGGDVTLOQTRYGDFQFALYKEGDPAPYKNPWRWRASFPFIITV 170



```
FT CONFLICT 53 53 L -> Q (in Ref. 3).
FT CONFLICT 61 61 D -> H (in Ref. 3).
FT CONFLICT 115 115 L -> M (in Ref. 3).
FT CONFLICT 120 120 A -> F (in Ref. 1).
FT CONFLICT 149 149 R -> G (in Ref. 1 and 3).
FT CONFLICT 175 175 G -> R (in Ref. 3).
FT CONFLICT 201 201 M -> T (in Ref. 3).
FT CONFLICT 252 252 D -> N (in Ref. 3).
FT CONFLICT 263 263 D -> A (in Ref. 3).
FT CONFLICT 268 268 P -> S (in Ref. 3).
FT CONFLICT 290 290 N -> H (in Ref. 1).
FT CONFLICT 417 417 V -> M (in Ref. 1).
FT CONFLICT 525 525 G -> R (in Ref. 1 and 3).
FT CONFLICT 561 561 P -> S (in Ref. 1 and 3).
SQ SEQUENCE 631 AA; 69233 MW; CC84A1762FC022DD CRC64;

Query Match 25.1%; Score 448; DB 1; Length 631;
Best Local Similarity 26.4%; Pred. No. 1.3e-24;
Matches 129; Conservative 45; Mismatches 87; Indels 228; Gaps 10;

Qy 1 MSPSPTALFCLGCLG-RVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQPGGVDLYRL 59
Db 1 MTPALTALCLGLSLGPRTRVQAGFPKPTLWABFGSVISWGSPVTIWCQGSLEAQEYQL 60
Qy 60 EKLSSSRVQD-----QAVLFIPAMKRSIAGRYCSYQNGSLWSLPSDLELVATGV 110
Db 61 DKESPEPLDRNNLEPKPKARFSPSWTQHAGRYCHYYSSAGWSEPSDPLELVMTGA 120
Qy 111 FAKPSLSAQPGPVGSSGDVTLQC--QTRY-----TPNSWDTCLLTR-----ETGLQDLALWDHTAQNLLRMGLAFLVLVALV 138
Db 121 YSKPTLSALPSPVVASGGMWTLRCGSKRYHHFVLMKEGEHQLPRTLDSQHLHSGGQAL 180
Qy 139 -----
Db 181 FPGVPVNPBHRWRTCYYYMYNTPRVMSHPDLEILLPSGVSRKPSLLITLQGPLAPQGS 240
Qy 139 -----GFDQFALYKEGD-----PAPYKNPE-----
Db 241 LTLCQGSVDGYDRFVLYKEGEGRDFLQRPQQPQAGLSQANFTLGPVSPSNGGQRCYGAH 300
Qy 159 ----RW-----
Db 301 NLSSEMSAPSDPLNLMAGIYDVTLSAQPGPTVASGENVTLCCSQMWQDFTLLTKEG 360
Qy 161 -----YPASPIITVTAHSGTTRCYFSRSDPYLWSAPSDPLELVVTG 204
Db 361 AAHPPLRLRSMYGAHKYQAEFPMSPTSAHAGTYRCYGSYSNPYLLSHHPSEPLELVVSG 420
Qy 205 TSVTPSRLPTPPSS--VAEFSATAELTVSTNKVF-----TTTSRSITTSKES 254
Db 421 HSGSSLPPTGPPSTPGLGRYLEVIGVSAFVLLFLLLFLLRQRHSHKRTSDQKRT 480
Qy 255 D--SPAGPA 261
Db 481 DFQRPAGAA 489

RESULT 13
Q8MI28 PRELIMINARY; PRT; 306 AA.
AC Q8MI28;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE NK946vl.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA LaBonte M.L., Miller J., Letvin N.L.;

Query Match 24.8%; Score 443; DB 2; Length 307;
Best Local Similarity 35.9%; Pred. No. 1.3e-24;
Matches 115; Conservative 40; Mismatches 119; Indels 46; Gaps 7;

Qy 1 MSPSPTALFCLGCLG-RVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQPGGVDLYRL 59
Db 1 MSSTLRALLCLGLCLSORISAPKOTLPKPIRAESTYMWPKKQATLCCQGSYGAVEYQL 60
Qy 60 -----EKLSSSRVQDQAVLFIPAMKRSIAGRYCSYQNGSLWSLPSDQLE 104
Db 61 HFEGSLFAVERPKPPERINGVKFH-----IPDMNSRKAGRYSCIYRVGELMSERSDLLD 114
Qy 105 LVATGVFAKPSLSAQPGPVGSSGDVTLQCTRYGDFQFALYKEGDPAKYKNPWRTRAS 164
Db 115 LVVTEMYDTPTLVHPGPEVTSGEKVTFCRLDTATSMFLLLKEGRSDVQRSYKQVQAE 174
Qy 165 FPIITVTAHSGTTRCYFSRSDPYLWSAPSDPLELVVTGTSVTPSRLPTPPSSVAEFS 224
Db 175 FPMGPVTTAHRGSYRC--FGSYNNYAWSFPSEPKVLLVTGDIENSTSLAPTDP----- 224
Qy 225 EATAELTVSTNKVFVTTETSRITTSKESDSPAGPARQYVTKGNLVRIICLGAVILIILA 284
Db 225 -----TPNSWDTCLLTR-----ETGLQDLALWDHTAQNLLRMGLAFLVLVALV 269
Qy 285 GFLEADWHSRRKRLRHRGRA 304
Db 270 CLLVEDWLSRKRTREQASRA 289

RESULT 14
Q8MI29 PRELIMINARY; PRT; 307 AA.
AC Q8MI29;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE NKp46.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA LaBonte M.L., Miller J., Letvin N.L.;

Query Match 24.8%; Score 443; DB 2; Length 307;
Best Local Similarity 35.9%; Pred. No. 1.3e-24;
Matches 115; Conservative 40; Mismatches 119; Indels 46; Gaps 7;

Qy 1 MSPSPTALFCLGCLG-RVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQPGGVDLYRL 59
Db 1 MSSTLRALLCLGLCLSORISAPKOTLPKPIRAESTYMWPKKQATLCCQGSYGAVEYQL 60
Qy 60 -----EKLSSSRVQDQAVLFIPAMKRSIAGRYCSYQNGSLWSLPSDQLE 104
Db 61 HFEGSLFAVERPKPPERINGVKFH-----IPDMNSRKAGRYSCIYRVGELMSERSDLLD 114
Qy 105 LVATGVFAKPSLSAQPGPVGSSGDVTLQCTRYGDFQFALYKEGDPAKYKNPWRTRAS 164
Db 115 LVVTEMYDTPTLVHPGPEVTSGEKVTFCRLDTATSMFLLLKEGRSDVQRSYKQVQAE 174
Qy 165 FPIITVTAHSGTTRCYFSRSDPYLWSAPSDPLELVVTGTSVTPSRLPTPPSSVAEFS 224
Db 175 FPMGPVTTAHRGSYRC--FGSYNNYAWSFPSEPKVLLVTGDIENSTSLAPTDP----- 224
Qy 225 EATAELTVSTNKVFVTTETSRITTSKESDSPAGPARQYVTKGNLVRIICLGAVILIILA 284
Db 225 -----TPNSWDTCLLTR-----ETGLQDLALWDHTAQNLLRMGLAFLVLVALV 269
Qy 285 GFLEADWHSRRKRLRHRGRA 304
Db 270 CLLVEDWLSRKRTREQASRA 289
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 115 LVWTEYDPTLSVHPGPEVTSGBKVTPTCYCLDTSATSMFLLLKGBSRDVRQSYGKVAE 174  
 165 PPIITVTAHSGTYRCYSFSDPVLWSAPSDPLELVVTSVTPSRLEPTEPPSSVAEFS 224  
 175 FPMGPVTAHSGYKRC--FGSYNNVAMSPFPSEPKLVGTGDIENSTLAPDTTP----- 227  
 225 BATAELTVSFTNKVFTTSTRTSITTSKESDPAGPARQYTYKGNLVRICIGAVILILA 284  
 228 -----TDSWDTCLLTRETG-----LQKDL-----ALWDHTAQNLRLMGLAFLVLVALV 270  
 285 GFLAEDWHSRRKRLRHGRA 304  
 271 CLLVEDWLSRKRTREQASRA 290

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 ID LIA4 HUMAN STANDARD; PRT; 499 AA.  
 AC P59901;  
 DT 10-OCT-2003 (Rel. 42, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Leukocyte immunoglobulin-like receptor subfamily A member 4 precursor  
 DE (immunoglobulin-like transcript 7) (ILT-7) (CD85g antigen).  
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 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Colonna M.;  
 RT "Immunoglobulin-like transcript 7,";  
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE OF 35-494 FROM N.A.  
 RA Canavez F.C.;  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP FUNCTION, AND TISSUE SPECIFICITY.  
 RX MEDLINE=22457157; PubMed=12529506; DOI=10.1073/pnas.0337567100;  
 RA Tedla N., Bandeira-Melo C., Tassinari P., Sloane D.E., Samplaski M.,  
 RA Cosman D., Borges L., Weller P.F., Arm J.P.;  
 RT "Activation of human eosinophils through leukocyte immunoglobulin-like  
 receptor 7,";  
 RL Proc. Natl. Acad. Sci. U.S.A. 100:1174-1179(2003).  
 CC -!- FUNCTION: May act as receptor for class I MHC antigens. Ligand  
 CC binding leads to the activation of eosinophils and to the release  
 CC of RNASE2, IL4 and leukotriene C4.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- TISSUE SPECIFICITY: Detected on eosinophils, neutrophils and  
 CC monocytes.  
 CC -!- SIMILARITY: Contains 4 immunoglobulin-like C2-type domains.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC  
 CC EMBL; AF041261; RAD02203.1; -;  
 DR EMBL; AF283989; AAL36993.1; -;  
 DR MIM; 607517; -;  
 DR InterPro; IPR003599; Ig.  
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 DR Pfam; PF00047; ig; 4  
 DR SMART; SM00409; Ig; 3.

PROSITE; PS0835; IG LIKE; 4.  
 KW Antigen; Glycoprotein; Immune response; Immunoglobulin domain;  
 KW Multigene family; Receptor; Repeat; Signal; Transmembrane.  
 FT SIGNAL 1 23 Potential.  
 FT CHAIN 24 499 Leukocyte immunoglobulin-like receptor  
 FT subfamily A member 4.  
 FT DOMAIN 24 446 Extracellular (Potential).  
 FT TRANSMEM 447 467 Potential.  
 FT DOMAIN 468 499 Cytoplasmic (Potential).  
 FT DOMAIN 24 118 Ig-like C2-type 1.  
 FT DOMAIN 123 213 Ig-like C2-type 2.  
 FT DOMAIN 224 313 Ig-like C2-type 3.  
 FT DOMAIN 324 413 Ig-like C2-type 4.  
 FT DISULFID 49 98 By similarity.  
 FT DISULFID 143 195 By similarity.  
 FT DISULFID 244 295 Potential.  
 FT CARBOHYD 344 395 Potential.  
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 FT CARBOHYD 300 300 N-linked (GlcNAc...) (Potential).  
 FT CONFLICT 398 398 T -> S (in Ref. 2).  
 SQ SEQUENCE 499 AA; 55096 MW; 387DA38D45183676 CRC64;

Query Match 24.8%; Score 442.5; DB 1; Length 499;  
 Best Local Similarity 26.6%; Pred. No. 2.6e-24;  
 Matches 126; Conservative 57; Mismatches 111; Indels 179; Gaps 9;

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 DB 120 YSRFTLSALPSPVTVSGVNVTLRCASRLGLGRFTLIEGDHRLSWTLNSHQHNGKFOAL 179  
 QY 165 PPIITVTAHSGTYRCYSFSDPVLWSAPSDPLELVVTSVTPSRLE----- 212  
 DB 180 FPMGPVTAHSGTYRCYSFSDPVLWSAPSDPLELVVTSVTPSRLE----- 239  
 QY 213 ----- 212  
 DB 240 LTQCGSDVGIVRYTYLYKEGADGLPQRPGRPOAGLSQANFTLSPVSRSYGQYRCYGAH 299  
 QY 213 -----PTBP-----PS-SV----- 220  
 DB 300 NVSSEWSPSPDLILAGQISDRPSLSVQPGVTVSGEKTLLCQSDPMPFTLLTKEG 359  
 QY 221 -----ABFSEATAELTVSFTNKVFTTETS----- 244  
 DB 360 AAHPPLRLRSMYGAHKYQAEFPMPSPVTSAAHAGTYRCYCTGRSSNPYLLSHSPSEPLEVVS 419  
 QY 245 --RSITTSKESDSDPAGPARQYTYKGNLVRICIGAVILILAAGLAEDWHSRR 295  
 DB 420 ATETLNPAQKSDSKTAPHLQDVTVENLIRMGVAGLVLLFLGILLFEAQHSQR 472

Search completed: October 29, 2005, 02:56:15  
 Job time : 178 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 29, 2005, 02:56:24 ; Search time 168 Seconds

(without alignments)  
843.551 Million cell updates/sec

Title: US-09-503-387-3

Perfect score: 1786

Sequence: 1 MSPSTALFCLGLGRVPA.....KSHGQDGRQDVHSGILCS 339

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1865214 seqs, 418043040 residues

Total number of hits satisfying chosen parameters: 1865214

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
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- 20: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1786	100.0	339	9	US-09-832-312-3
2	1786	100.0	339	11	US-09-829-495-3
3	1786	100.0	339	14	US-10-157-031-387
4	1786	100.0	339	16	US-10-850-034-3
5	1782	99.8	339	9	US-09-832-312-34
6	1782	99.8	339	9	US-09-832-312-36
7	1782	99.8	339	9	US-09-832-312-38
8	1782	99.8	339	9	US-09-832-312-40
9	1782	99.8	339	11	US-09-829-495-34
10	1782	99.8	339	11	US-09-829-495-36
11	1782	99.8	339	11	US-09-829-495-38

12	1782	99.8	339	11	US-09-829-495-40
13	1782	99.8	339	16	US-10-850-034-34
14	1782	99.8	339	16	US-10-850-034-36
15	1782	99.8	339	16	US-10-850-034-38
16	1782	99.8	339	16	US-10-850-034-40
17	1759	98.5	339	14	US-10-446-826-5
18	1759	98.5	339	16	US-10-446-826-5
19	1678	94.0	319	9	US-09-832-312-5
20	1678	94.0	319	11	US-09-829-495-5
21	1678	94.0	319	16	US-10-850-034-5
22	1672	93.6	321	16	US-10-741-601-402
23	1672	93.6	321	17	US-10-741-600-1204
24	1412	79.1	504	17	US-10-489-053-1
25	1346	75.4	620	16	US-10-741-601-403
26	1346	75.4	620	17	US-10-741-600-1205
27	1311	73.4	501	16	US-10-483-810-1
28	1307.5	73.2	512	16	US-10-483-810-2
29	1304	73.0	249	9	US-09-832-312-9
30	1304	73.0	249	11	US-09-829-495-9
31	1304	73.0	249	16	US-10-850-034-9
32	1304	73.0	369	14	US-10-446-826-37
33	1304	73.0	369	16	US-10-446-826-37
34	1122	62.8	313	9	US-09-832-312-16
35	1122	62.8	313	9	US-09-832-312-48
36	1122	62.8	313	11	US-09-829-495-16
37	1122	62.8	313	11	US-09-829-495-48
38	1122	62.8	313	16	US-10-850-034-16
39	1122	62.8	313	16	US-10-850-034-48
40	1118	62.6	313	9	US-09-832-312-42
41	1118	62.6	313	9	US-09-832-312-44
42	1118	62.6	313	11	US-09-829-495-42
43	1118	62.6	313	11	US-09-829-495-44
44	1118	62.6	313	11	US-09-829-495-44
45	1118	62.6	313	11	US-09-829-495-46

ALIGNMENTS

RESULT 1  
US-09-832-312-3  
; Sequence 3, Application US/09832312  
; Patent No. US20010049829A1  
; GENERAL INFORMATION:  
; APPLICANT: Bugfield et al.  
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF  
; FILE REFERENCE: 7853-234  
; CURRENT FILING DATE: 2001-04-09  
; CURRENT APPLICATION NUMBER: US/09/832,312  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: 09/610,118  
; PRIOR FILING DATE: 2000-02-14  
; PRIOR APPLICATION NUMBER: 09/503,387  
; PRIOR FILING DATE: 1999-12-06  
; PRIOR APPLICATION NUMBER: 09/454,824  
; PRIOR FILING DATE: 1999-12-06  
; PRIOR APPLICATION NUMBER: 09/345,468  
; PRIOR FILING DATE: 1999-06-30  
; NUMBER OF SEQ ID NOS: 78  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 339  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-832-312-3

Query Match 100.0%; Score 1786; DB 9; Length 339;  
Best Local Similarity 100.0%; Pred. No. 2,4e-128;  
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MSPSTALFCLGLGRVPAQSGPLPKPSLQALPSSLVPLEKVTLCRCQPGVDLYRLE 60  
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QY 241 TETSRITTSKESDSPAGPARQYTTKGNLVRCILGAVILIILAGFLAEDWHSRRKRLRH 300
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Db 301 RGRAVQRPPLPPLPQTRKSHGGDGRQDVHSRGLCS 339

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US-09-829-495-3
; Sequence 3, Application US/09829495
; Publication No. US20040001826A1
; GENERAL INFORMATION:
; APPLICANT: Busfield SJ
; APPLICANT: Villevall J
; APPLICANT: Jandrot-Perrus M
; APPLICANT: Vainchenker W
; APPLICANT: Gill DS
; APPLICANT: Qian MD
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/829,495
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-829-495-3

Query Match 100.0%; Score 1786; DB 11; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.4e-128;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
US-10-157-031-387
; Sequence 387, Application US/10157031
; Publication No. US20030108890A1
; GENERAL INFORMATION:
; APPLICANT: Baranova, A. V.
; APPLICANT: Yankovsky, N. K.
; APPLICANT: Kozlov, A. P.
; APPLICANT: Lobashev, A. V.
; APPLICANT: Krukovskaya, L. L.
; TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequences
; FILE REFERENCE: 2760-103
; CURRENT APPLICATION NUMBER: US/10/157,031
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 415
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 387
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-157-031-387

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Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 KLSRRYQDQAVLFIPAMKRSIAGRYCSYONGSLWSLPDQLELVATGVFAKPSLSAQP 120
Db 61 KLSRRYQDQAVLFIPAMKRSIAGRYCSYONGSLWSLPDQLELVATGVFAKPSLSAQP 120
QY 121 GPAVSSGGDVTLCQCTRYGDFQFALYKEGDPAPYKPNRWYRASFPITVTTAAHSGTYRC 180
Db 121 GPAVSSGGDVTLCQCTRYGDFQFALYKEGDPAPYKPNRWYRASFPITVTTAAHSGTYRC 180
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QY 241 TETSRITTSKESDSPAGPARQYTTKGNLVRCILGAVILIILAGFLAEDWHSRRKRLRH 300
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RESULT 4
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; Sequence 3, Application US/10850034
; Publication No. US20040253236A1
; GENERAL INFORMATION:
; APPLICANT: Busfield SJ
; APPLICANT: Villevall J
; APPLICANT: Jandrot-Perrus M
; APPLICANT: Vainchenker W
; APPLICANT: Gill DS
; APPLICANT: Qian MD
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/10/850,034
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RESULT 3
US-10-157-031-387
; Sequence 387, Application US/10157031
; Publication No. US20030108890A1
; GENERAL INFORMATION:
; APPLICANT: Baranova, A. V.
; APPLICANT: Yankovsky, N. K.
; APPLICANT: Kozlov, A. P.
; APPLICANT: Lobashev, A. V.
; APPLICANT: Krukovskaya, L. L.
; TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequences
; FILE REFERENCE: 2760-103
; CURRENT APPLICATION NUMBER: US/10/157,031
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 415
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 387
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-157-031-387

Query Match 100.0%; Score 1786; DB 14; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.4e-128;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 181 YFSRRDPYLWSAPSDPLELVVTGTSVTPSRLPTEPPSSVAEFSATAELTVSFTNKVFT 240
Db 181 YFSRRDPYLWSAPSDPLELVVTGTSVTPSRLPTEPPSSVAEFSATAELTVSFTNKVFT 240
QY 241 TETSRITTSKESDSPAGPARQYTTKGNLVRCILGAVILIILAGFLAEDWHSRRKRLRH 300
Db 241 TETSRITTSKESDSPAGPARQYTTKGNLVRCILGAVILIILAGFLAEDWHSRRKRLRH 300

RESULT 4
US-10-850-034-3
; Sequence 3, Application US/10850034
; Publication No. US20040253236A1
; GENERAL INFORMATION:
; APPLICANT: Busfield SJ
; APPLICANT: Villevall J
; APPLICANT: Jandrot-Perrus M
; APPLICANT: Vainchenker W
; APPLICANT: Gill DS
; APPLICANT: Qian MD
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/10/850,034
```

```
; CURRENT FILING DATE: 2004-05-20
; PRIOR APPLICATION NUMBER: US/09/829,495
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-850-034-3

Query Match      100.0%; Score 1786; DB 16; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.4e-128;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPSPALFCLGLCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPFGVDLYRLE 60
DB 1 MSPSPALFCLGLCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPFGVDLYRLE 60
QY 61 KLSSSRYQDQAVLFIIPAMKRSIAGRYCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQ 120
DB 61 KLSSSRYQDQAVLFIIPAMKRSIAGRYCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQ 120
QY 121 GPAVSSGGDVTLCQTRYGFDPQALYKEGDPAPYKPNRWYRASFPFIITVTAHSGTYRC 180
DB 121 GPAVSSGGDVTLCQTRYGFDPQALYKEGDPAPYKPNRWYRASFPFIITVTAHSGTYRC 180
QY 181 YSFSSRDPLYMSAPSDPLELVVTGTSVTPSRLPTEPPSSVAEFSATAELTVSFTNKVFT 240
DB 181 YSFSSRDPLYMSAPSDPLELVVTGTSVTPSRLPTEPPSSVAEFSATAELTVSFTNKVFT 240
QY 241 TETSRITTSKPESDSPAGPARQYTKGNLVRIICLGAVALIILAGFLAEDWHSRRKRLRH 300
DB 241 TETSRITTSKPESDSPAGPARQYTKGNLVRIICLGAVALIILAGFLAEDWHSRRKRLRH 300
QY 301 RGRAVORPLPPLPQTRKSHGGQDGGQDVHSRGLCS 339
DB 301 RGRAVORPLPPLPQTRKSHGGQDGGQDVHSRGLCS 339

RESULT 6
US-09-832-312-36
; Sequence 36, Application US/09832312
; Patent No. US20010049829A1
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-832-312-36

Query Match      99.8%; Score 1782; DB 9; Length 339;
Best Local Similarity 99.7%; Pred. No. 4.8e-128;
Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSPSPALFCLGLCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPFGVDLYRLE 60
DB 1 MSPSPALFCLGLCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPFGVDLYRLE 60
QY 61 KLSSSRYQDQAVLFIIPAMKRSIAGRYCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQ 120
DB 61 KLSSSRYQDQAVLFIIPAMKRSIAGRYCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQ 120
QY 121 GPAVSSGGDVTLCQTRYGFDPQALYKEGDPAPYKPNRWYRASFPFIITVTAHSGTYRC 180
DB 121 GPAVSSGGDVTLCQTRYGFDPQALYKEGDPAPYKPNRWYRASFPFIITVTAHSGTYRC 180
QY 181 YSFSSRDPLYMSAPSDPLELVVTGTSVTPSRLPTEPPSSVAEFSATAELTVSFTNKVFT 240
DB 181 YSFSSRDPLYMSAPSDPLELVVTGTSVTPSRLPTEPPSSVAEFSATAELTVSFTNKVFT 240

RESULT 5
US-09-832-312-34
; Sequence 34, Application US/09832312
; Patent No. US20010049829A1
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 34
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-832-312-34
```

```
Db      181 YFSRSDPYLWASPDPLELVVTGTSVTPSRLPTEPPSSVAEFSATAELTVSFNKNVFT 240
QY      241 TETSRITTSKPESDSPAGPARQYTKGNLVICLGVAVILIILAGFLAEDWHSRRKRLRH 300
Db      241 TETSRITTSKPESDSPAGPARQYTKGNLVICLGVAVILIILAGFLAEDWHSRRKRLRH 300
QY      301 RGRAVQRLPPLPPLPQTRKSHGGQDGRQDVHSRGLCS 339
Db      301 RGRAVQRLPPLPPLPQTRKSHGGQDGRQDVHSRGLCS 339

RESULT 7
US-09-832-312-38
; Sequence 38, Application US/09832312
; Patent No. US20010049829A1
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 38
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-312-40
```

```
Query Match      99.8%; Score 1782; DB 9; Length 339;
Best Local Similarity 99.7%; Pred. No. 4.8e-128;
Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 MSPSPTALFCLGLCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRLE 60
Db      1 MSPSPTALFCLGLCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRLE 60
QY      61 KLSRSRYQDQAVLFIPAMKRSLAGRYCSYQNGSLWSPSDQLELVATGVFAKPSLSAQP 120
Db      61 KLSRSRYQDQAVLFIPAMKRSLAGRYCSYQNGSLWSPSDQLELVATGVFAKPSLSAQP 120
QY      121 GPAVSSGGDVTLLQCQTRYGDFQFALYKEGDPAPYKNPERWYRASPPITVTAHSGTYRC 180
Db      121 GPAVSSGGDVTLLQCQTRYGDFQFALYKEGDPAPYKNPERWYRASPPITVTAHSGTYRC 180
QY      181 YFSRSDPYLWASPDPLELVVTGTSVTPSRLPTEPPSSVAEFSATAELTVSFNKNVFT 240
Db      181 YFSRSDPYLWASPDPLELVVTGTSVTPSRLPTEPPSSVAEFSATAELTVSFNKNVFT 240
QY      241 TETSRITTSKPESDSPAGPARQYTKGNLVICLGVAVILIILAGFLAEDWHSRRKRLRH 300
Db      241 TETSRITTSKPESDSPAGPARQYTKGNLVICLGVAVILIILAGFLAEDWHSRRKRLRH 300

RESULT 8
US-09-832-312-40
; Sequence 40, Application US/09832312
; Patent No. US20010049829A1
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
```

```
Query Match      99.8%; Score 1782; DB 9; Length 339;
Best Local Similarity 99.7%; Pred. No. 4.8e-128;
Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 MSPSPTALFCLGLCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRLE 60
Db      1 MSPSPTALFCLGLCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRLE 60
QY      61 KLSRSRYQDQAVLFIPAMKRSLAGRYCSYQNGSLWSPSDQLELVATGVFAKPSLSAQP 120
Db      61 KLSRSRYQDQAVLFIPAMKRSLAGRYCSYQNGSLWSPSDQLELVATGVFAKPSLSAQP 120
QY      121 GPAVSSGGDVTLLQCQTRYGDFQFALYKEGDPAPYKNPERWYRASPPITVTAHSGTYRC 180
Db      121 GPAVSSGGDVTLLQCQTRYGDFQFALYKEGDPAPYKNPERWYRASPPITVTAHSGTYRC 180
QY      181 YFSRSDPYLWASPDPLELVVTGTSVTPSRLPTEPPSSVAEFSATAELTVSFNKNVFT 240
Db      181 YFSRSDPYLWASPDPLELVVTGTSVTPSRLPTEPPSSVAEFSATAELTVSFNKNVFT 240
QY      241 TETSRITTSKPESDSPAGPARQYTKGNLVICLGVAVILIILAGFLAEDWHSRRKRLRH 300
Db      241 TETSRITTSKPESDSPAGPARQYTKGNLVICLGVAVILIILAGFLAEDWHSRRKRLRH 300

RESULT 9
US-09-829-495-34
; Sequence 34, Application US/09829495
; Publication No. US20040001826A1
; GENERAL INFORMATION:
; APPLICANT: Busfield SJ
; APPLICANT: Villieval J
; APPLICANT: Jandrot-Perrus M
; APPLICANT: Vainchenker W
; APPLICANT: Gill DS
; APPLICANT: Qian MD
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/829,495
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
```

```
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 40
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-312-40
```

```
Query Match      99.8%; Score 1782; DB 9; Length 339;
Best Local Similarity 99.7%; Pred. No. 4.8e-128;
Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 MSPSPTALFCLGLCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRLE 60
Db      1 MSPSPTALFCLGLCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRLE 60
QY      61 KLSRSRYQDQAVLFIPAMKRSLAGRYCSYQNGSLWSPSDQLELVATGVFAKPSLSAQP 120
Db      61 KLSRSRYQDQAVLFIPAMKRSLAGRYCSYQNGSLWSPSDQLELVATGVFAKPSLSAQP 120
QY      121 GPAVSSGGDVTLLQCQTRYGDFQFALYKEGDPAPYKNPERWYRASPPITVTAHSGTYRC 180
Db      121 GPAVSSGGDVTLLQCQTRYGDFQFALYKEGDPAPYKNPERWYRASPPITVTAHSGTYRC 180
QY      181 YFSRSDPYLWASPDPLELVVTGTSVTPSRLPTEPPSSVAEFSATAELTVSFNKNVFT 240
Db      181 YFSRSDPYLWASPDPLELVVTGTSVTPSRLPTEPPSSVAEFSATAELTVSFNKNVFT 240
QY      241 TETSRITTSKPESDSPAGPARQYTKGNLVICLGVAVILIILAGFLAEDWHSRRKRLRH 300
Db      241 TETSRITTSKPESDSPAGPARQYTKGNLVICLGVAVILIILAGFLAEDWHSRRKRLRH 300
QY      301 RGRAVQRLPPLPPLPQTRKSHGGQDGRQDVHSRGLCS 339
Db      301 RGRAVQRLPPLPPLPQTRKSHGGQDGRQDVHSRGLCS 339
```

```
RESULT 9
US-09-829-495-34
; Sequence 34, Application US/09829495
; Publication No. US20040001826A1
; GENERAL INFORMATION:
; APPLICANT: Busfield SJ
; APPLICANT: Villieval J
; APPLICANT: Jandrot-Perrus M
; APPLICANT: Vainchenker W
; APPLICANT: Gill DS
; APPLICANT: Qian MD
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/829,495
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
```

```
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 34
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-829-495-34

Query Match          99.8%; Score 1782; DB 11; Length 339;
Best Local Similarity 99.7%; Pred. No. 4.8e-128;
Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSPSPALFCLGLCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPVGVDLYRLE 60
Db 1 MSPSPALFCLGLCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPVGVDLYRLE 60
QY 61 KLSRRYQDQAVLFIIPAMKRSIAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQ 120
Db 61 KLSRRYQDQAVLFIIPAMKRSIAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQ 120
QY 121 GPVSSGGDVTLCQCTRYGDFQFALYKEGDPAPYKPNRWYRASPPITVTAHSGTYRC 180
Db 121 GPVSSGGDVTLCQCTRYGDFQFALYKEGDPAPYKPNRWYRASPPITVTAHSGTYRC 180
QY 181 YFSRRDPYLWSAPSDPLELVVTGTSVTPSRPTEPPSSVAEFSSEATAELTVSFTNKVFT 240
Db 181 YFSRRDPYLWSAPSDPLELVVTGTSVTPSRPTEPPSSVAEFSSEATAELTVSFTNKVFT 240
QY 241 TETSRITSPKESDSPAGPARQYTKGNLVICLGVILIIILAGFLAEDWHSRRKRLRH 300
Db 241 TETSRITSPKESDSPAGPARQYTKGNLVICLGVILIIILAGFLAEDWHSRRKRLRH 300
QY 301 RGRAVORPLPLPPLPQTRKSHGGQDGRQDVHSRGLCS 339
Db 301 RGRAVORPLPLPPLPQTRKSHGGQDGRQDVHSRGLCS 339

RESULT 11
US-09-829-495-38
; Sequence 38, Application US/09829495
; Publication No. US20040001826A1
; GENERAL INFORMATION:
; APPLICANT: Busfield SJ
; APPLICANT: Villevall J
; APPLICANT: Gandrot-Perrus M
; APPLICANT: Vainchenker W
; APPLICANT: Gill DS
; APPLICANT: Qian MD
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/829,495
; PRIOR FILING DATE: 2001-04-09
; PRIOR FILING DATE: 2000-06-30
; PRIOR FILING DATE: 2000-02-14
; PRIOR FILING DATE: 1999-12-06
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 38
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-829-495-38

Query Match          99.8%; Score 1782; DB 11; Length 339;
Best Local Similarity 99.7%; Pred. No. 4.8e-128;
Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSPSPALFCLGLCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPVGVDLYRLE 60
Db 1 MSPSPALFCLGLCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPVGVDLYRLE 60
QY 61 KLSRRYQDQAVLFIIPAMKRSIAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQ 120
Db 61 KLSRRYQDQAVLFIIPAMKRSIAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQ 120
QY 121 GPVSSGGDVTLCQCTRYGDFQFALYKEGDPAPYKPNRWYRASPPITVTAHSGTYRC 180
Db 121 GPVSSGGDVTLCQCTRYGDFQFALYKEGDPAPYKPNRWYRASPPITVTAHSGTYRC 180
QY 181 YFSRRDPYLWSAPSDPLELVVTGTSVTPSRPTEPPSSVAEFSSEATAELTVSFTNKVFT 240
Db 181 YFSRRDPYLWSAPSDPLELVVTGTSVTPSRPTEPPSSVAEFSSEATAELTVSFTNKVFT 240

; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-829-495-36

Query Match          99.8%; Score 1782; DB 11; Length 339;
Best Local Similarity 99.7%; Pred. No. 4.8e-128;
Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSPSPALFCLGLCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPVGVDLYRLE 60
Db 1 MSPSPALFCLGLCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPVGVDLYRLE 60
QY 61 KLSRRYQDQAVLFIIPAMKRSIAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQ 120
Db 61 KLSRRYQDQAVLFIIPAMKRSIAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQ 120
QY 121 GPVSSGGDVTLCQCTRYGDFQFALYKEGDPAPYKPNRWYRASPPITVTAHSGTYRC 180
Db 121 GPVSSGGDVTLCQCTRYGDFQFALYKEGDPAPYKPNRWYRASPPITVTAHSGTYRC 180
QY 181 YFSRRDPYLWSAPSDPLELVVTGTSVTPSRPTEPPSSVAEFSSEATAELTVSFTNKVFT 240
Db 181 YFSRRDPYLWSAPSDPLELVVTGTSVTPSRPTEPPSSVAEFSSEATAELTVSFTNKVFT 240

; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 34
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-829-495-34

Query Match          99.8%; Score 1782; DB 11; Length 339;
Best Local Similarity 99.7%; Pred. No. 4.8e-128;
Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSPSPALFCLGLCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPVGVDLYRLE 60
Db 1 MSPSPALFCLGLCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPVGVDLYRLE 60
QY 61 KLSRRYQDQAVLFIIPAMKRSIAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQ 120
Db 61 KLSRRYQDQAVLFIIPAMKRSIAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQ 120
QY 121 GPVSSGGDVTLCQCTRYGDFQFALYKEGDPAPYKPNRWYRASPPITVTAHSGTYRC 180
Db 121 GPVSSGGDVTLCQCTRYGDFQFALYKEGDPAPYKPNRWYRASPPITVTAHSGTYRC 180
QY 181 YFSRRDPYLWSAPSDPLELVVTGTSVTPSRPTEPPSSVAEFSSEATAELTVSFTNKVFT 240
Db 181 YFSRRDPYLWSAPSDPLELVVTGTSVTPSRPTEPPSSVAEFSSEATAELTVSFTNKVFT 240
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```
QY 241 TETSRITTSKESDSPAGPARQYTKGNLVRLICGAVILIIAGFLAEDWHSRRKRLRH 300
Db 241 TETSRITTSKESDSPAGPARQYTKGNLVRLICGAVILIIAGFLAEDWHSRRKRLRH 300
QY 301 RGRAVORPLPPLPQTRKSHGGDGGGRQDVHSRGLCS 339
Db 301 RGRAVORPLPPLPQTRKSHGGDGGGRQDVHSRGLCS 339

RESULT 12
US-09-829-495-40
; Sequence 40, Application US/09829495
; Publication No. US20040001826A1
; GENERAL INFORMATION:
; APPLICANT: Busfield SJ
; APPLICANT: Villevall J
; APPLICANT: Jandrot-Perrus M
; APPLICANT: Vainchenker W
; APPLICANT: Gill DS
; APPLICANT: Qian MD
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/829,495
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 40
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-829-495-40

Query Match 99.8%; Score 1782; DB 11; Length 339;
Best Local Similarity 99.7%; Pred. No. 4.8e-128;
Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSPSPTALFCLGCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQPGVDLYRLE 60
Db 1 MSPSPTALFCLGCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQPGVDLYRLE 60
QY 61 KLSRSRYQDQAVLFTIPAMKRSAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQ 120
Db 61 KLSRSRYQDQAVLFTIPAMKRSAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQ 120
QY 121 GPVSSGGDVTLLQCTRYGDFQFALYKEGDPAKYKNPERWYRASPIITVTAHSGTYRC 180
Db 121 GPVSSGGDVTLLQCTRYGDFQFALYKEGDPAKYKNPERWYRASPIITVTAHSGTYRC 180
QY 181 YSFSSRDPLYMSAPSDPLELVVTGTSVTPSRLPTEPPSSVAEFSSEATAELTVSFTNKVFT 240
Db 181 YSFSSRDPLYMSAPSDPLELVVTGTSVTPSRLPTEPPSSVAEFSSEATAELTVSFTNKVFT 240
QY 241 TETSRITTSKESDSPAGPARQYTKGNLVRLICGAVILIIAGFLAEDWHSRRKRLRH 300
Db 241 TETSRITTSKESDSPAGPARQYTKGNLVRLICGAVILIIAGFLAEDWHSRRKRLRH 300
QY 301 RGRAVORPLPPLPQTRKSHGGDGGGRQDVHSRGLCS 339
Db 301 RGRAVORPLPPLPQTRKSHGGDGGGRQDVHSRGLCS 339

RESULT 13
US-10-850-034-34
; Sequence 34, Application US/10850034
; Publication No. US20040253236A1
; GENERAL INFORMATION:
; APPLICANT: Busfield SJ
; APPLICANT: Villevall J
; APPLICANT: Jandrot-Perrus M
; APPLICANT: Vainchenker W
; APPLICANT: Gill DS
; APPLICANT: Qian MD
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/10/850,034
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Publication No. US20040253236A1
; GENERAL INFORMATION:
; APPLICANT: Busfield SJ
; APPLICANT: Villevall J
; APPLICANT: Jandrot-Perrus M
; APPLICANT: Vainchenker W
; APPLICANT: Gill DS
; APPLICANT: Qian MD
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/10/850,034
; CURRENT FILING DATE: 2004-05-20
; PRIOR APPLICATION NUMBER: US/09/829,495
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 34
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-850-034-34

Query Match 99.8%; Score 1782; DB 16; Length 339;
Best Local Similarity 99.7%; Pred. No. 4.8e-128;
Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSPSPTALFCLGCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQPGVDLYRLE 60
Db 1 MSPSPTALFCLGCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQPGVDLYRLE 60
QY 61 KLSRSRYQDQAVLFTIPAMKRSAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQ 120
Db 61 KLSRSRYQDQAVLFTIPAMKRSAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQ 120
QY 121 GPVSSGGDVTLLQCTRYGDFQFALYKEGDPAKYKNPERWYRASPIITVTAHSGTYRC 180
Db 121 GPVSSGGDVTLLQCTRYGDFQFALYKEGDPAKYKNPERWYRASPIITVTAHSGTYRC 180
QY 181 YSFSSRDPLYMSAPSDPLELVVTGTSVTPSRLPTEPPSSVAEFSSEATAELTVSFTNKVFT 240
Db 181 YSFSSRDPLYMSAPSDPLELVVTGTSVTPSRLPTEPPSSVAEFSSEATAELTVSFTNKVFT 240
QY 241 TETSRITTSKESDSPAGPARQYTKGNLVRLICGAVILIIAGFLAEDWHSRRKRLRH 300
Db 241 TETSRITTSKESDSPAGPARQYTKGNLVRLICGAVILIIAGFLAEDWHSRRKRLRH 300
QY 301 RGRAVORPLPPLPQTRKSHGGDGGGRQDVHSRGLCS 339
Db 301 RGRAVORPLPPLPQTRKSHGGDGGGRQDVHSRGLCS 339

RESULT 14
US-10-850-034-36
; Sequence 36, Application US/10850034
; Publication No. US20040253236A1
; GENERAL INFORMATION:
; APPLICANT: Busfield SJ
; APPLICANT: Villevall J
; APPLICANT: Jandrot-Perrus M
; APPLICANT: Vainchenker W
; APPLICANT: Gill DS
; APPLICANT: Qian MD
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/10/850,034
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GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: October 29, 2005, 02:47:38 ; Search time 39 Seconds  
(without alignments)  
836.346 Million cell updates/sec

Title: US-09-503-387-3  
Perfect score: 1796  
Sequence: 1 MSPSPALFCLGLCLGRVPA.....KSHGQDGRQDVHSGRLCS 339

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1786	100.0	339	JC7509	glycoprotein VI-1
2	428.5	24.0	466	JCS897	killer cell inhibi
3	426.5	23.9	264	I46020	PC gamma 2 recepto
4	392	21.9	287	JH0132	IgA (Fc) receptor.
5	372.5	20.9	841	JCS894	killer cell inhibi
6	365.5	20.5	635	JCS896	killer cell inhibi
7	358.5	20.1	239	G02630	Fc alpha-1-2-3
8	356.5	20.0	680	JCS895	killer cell inhibi
9	335	18.8	444	G01925	KIR (cl-11) NK rec
10	330	18.5	296	B53434	cell surface glyco
11	328	18.4	348	A56247	natural killer cel
12	327	18.3	444	G01924	KIR (cl-2) NK rece
13	323.5	18.1	341	I61725	natural killer ass
14	322	18.0	1327	T09402	immunoglobulin-lik
15	317.5	17.8	335	A53434	cell surface glyco
16	316	17.7	455	G01923	KIR (cl-5) NK rece
17	315	17.6	427	G02034	killer cell inhibi
18	289.5	16.2	303	A40807	membrane glycoprot
19	182	10.2	184	T46433	hypothetical prote
20	145	8.1	237	A42013	alpha-1-B-glycopro
21	142.5	8.0	474	OMHU1B	alpha-1-B-glycopro
22	126.5	7.1	3707	I51825	heparan sulfate pr
23	124.5	7.0	267	I56110	Fc-gamma RIIB-ali
24	118.5	6.6	267	A35902	Fc gamma (19G) rec
25	118	6.6	4391	A38096	perlecan precursor
26	116	6.5	2774	A43359	microtubule-associ
27	115	6.4	283	1 FCM5G1	Fc gamma (19G) rec
28	114.5	6.4	1259	A43425	Bravo/Nr-CAM cell
29	113.5	6.4	592	D70863	hypothetical prote

30	113.5	6.4	1268	1	A39640	neural cell adhesi
31	110.5	6.2	1612	2	T30805	ducl1 protein - mo
32	110	6.2	270	2	A34636	Fc-gamma receptor
33	109.5	6.1	4162	2	T42633	connectin/titin -
34	108	6.0	257	2	S00682	IgE Fc receptor al
35	107	6.0	261	2	S29360	Fc gamma (19G) rec
36	106.5	6.0	3375	2	T19821	hypothetical prote
37	106	5.9	285	2	S36903	Fc gamma (19G) rec
38	106	5.9	739	2	JN0581	vascular cell adhe
39	106	5.9	931	2	T49710	related to glucan
40	106	5.9	1607	2	T02837	long chain fatty a
41	105.5	5.9	330	2	A40071	Fc gamma (19G) rec
42	105.5	5.9	330	2	I49660	Fc-gamma-1/gamma-2
43	104.5	5.9	267	2	I72882	Fc gamma receptor
44	104.5	5.9	1651	2	T14160	transmembrane rece
45	104	5.8	1367	1	S48478	glucan 1,4-alpha-g

ALIGNMENTS

RESULT 1

JC7509  
glycoprotein VI-1 - human  
C:Species: Homo sapiens (man)  
C:Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 09-Jul-2004  
C:Accession: JC7509; PC7101  
R:Etzumi, Y.; Uchiyama, T.; Takayama, H.  
Biochem. Biophys. Res. Commun. 277, 27-36, 2000  
A:Title: Molecular cloning, genomic structure, chromosomal localization, and alternative  
A:Reference number: JC7509; MUID:20483673; PMID:11027634  
A:Contents: Platelet  
A:Accession: JC7509  
A:Molecule type: mRNA  
A:Residues: 1-339 <E2>  
A:Cross-references: UNIPROT:Q9UIP2; DDBJ:AB043819  
A:Accession: PC7101  
A:Molecule type: Protein  
A:Residues: 28-41;62-79;114-142 <E2>  
C:Comment: This protein, which belongs to the immunoglobulin superfamily, is the major c  
or gamma chain as a signal transducing subunit, and plays some roles in cancer cells.  
C:Genetics:  
A:Gene: gpVI-1  
A:Map position: 19q13.4  
A:Introns: 62/1; 95/1; 353/1; 638/1; 692/1; 752/1; 803/1  
C:Keywords: Glycoprotein; immunoglobulin; platelet

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Best Local Similarity	100.0%;	Pred. No. 5.8e-122;		
Matches 339;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MSPSPTALFCLGICLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCOGPPGVVDLVRL	60	
Db	1	MSPSPTALFCLGICLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCOGPPGVVDLVRL	60	
Qy	61	KLSSRYQDAVLFPAMKRSLAGRVCSYQNGSLWSPDQDLQDLVATGVFAKPSLSAQP	120	
Db	61	KLSSRYQDAVLFPAMKRSLAGRVCSYQNGSLWSPDQDLQDLVATGVFAKPSLSAQP	120	
Qy	121	GPAVSSGGDVTLQCQTRYGDFQFALYKEGDPAPYKKNPERWYRASFPITITVAHSGTYRC	180	
Db	121	GPAVSSGGDVTLQCQTRYGDFQFALYKEGDPAPYKKNPERWYRASFPITITVAHSGTYRC	180	
Qy	181	YFSSRDPLWAPSDDPLVLTGTSVTSRSLPTEPPSSVAEPSEATBLTFSFTNKVFT	240	
Db	181	YFSSRDPLWAPSDDPLVLTGTSVTSRSLPTEPPSSVAEPSEATBLTFSFTNKVFT	240	
Qy	241	TETSRITTSKPESDSPAGPAQYTKGNLVRICLGAIVILIIILAGFLAEDWHRRKRLRH	300	
Db	241	TETSRITTSKPESDSPAGPAQYTKGNLVRICLGAIVILIIILAGFLAEDWHRRKRLRH	300	
Qy	301	RGRVQRPLPPLPQTRKSHGQDGRQDVHSGRLCS	339	

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Db 301 RGRAVQRLPPLPPLPQTRKSHGQDGRQDVHSGILCS 339
RESULT 2
JC5897
killer cell inhibitory receptor p91 precursor - human
C;Species: Homo sapiens (man)
C;Date: 18-Mar-1998 #sequence_revision 18-Mar-1998 #text_change 05-Nov-1999
C;Accession: JC5897
R;Yamashita, Y.; Fukuta, D.; Teuji, A.; Nagabukuro, A.; Matsuda, Y.; Nishikawa, Y.; Ohya
J. Biochem. 123, 358-368, 1998
A;Title: Genomic structures and chromosomal location of p91, a novel murine regulatory r
A;Reference number: JC5894; MUID:98218758; PMID:9538215
A;Accession: JC5897
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-466 <YAM>
A;Cross-references: GB:AF041034; NID:g2791689; PIDN:AAB96926.1; PID:g2791690
C;Comment: This protein function as inhibitory cell-surface molecule against cell activa
C;Genetics:
F;1-23/Domain: signal sequence #status predicted <SIG>
Query Match 24.0%; Score 428.5; DB 2; Length 466;
Best Local Similarity 36.1%; Pred. No. 1.4e-23;
Matches 126; Conservative 43; Mismatches 127; Indels 53; Gaps 13;
Qy 1 MSPSPTALFCLGLCLG-RVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVD---L 56
Db 1 MTPILTVLICGLSLGPRTHVQAGHLKPTLWAEPSGVIIQSGSPVTLRCQGSQAEEVHL 60
Qy 57 YRLKLS--GRYQD---QAVLFIPAMKRSIAGRYCSYQNGSLWSLSQLELVATGVF 111
Db 61 YRENKASWVRRIQPGKNGQFPISITWEHAGRYHCQYGHNSSEYSDPLELVVTGAY 120
Qy 112 AKPSLSAQPGAVSSGGDVTLQCTRYGDFQFALYKEGDPAPYKKNPERW-----YR 162
Db 121 SKPTLSLPSVPVTLGGNVTLQCVSAFDGFIKCEGED---EHPQLNHSRHARGSSR 177
Qy 163 ASFPITITAAHSGTYRCYSFSSRDPYLWSAPSDPLELVVTGTSVTPSRLETPSPSSVAE 222
Db 178 AIFSFGVSPNRRWSHRCYGYDLSNPVWSPPSDLELLVPGVSKKPS-LSVQPGPVVAP 236
Qy 223 FSEATAELT--VSFTNKVFTTTSRITTSKPSDSAPAGRAYTYTKGNLVRI-----C 274
Db 237 GESLTQCVSDVGYDRFVLYKEGERDLRLQRPQ-Q-AGLSQANFTLGPVRSRYGGQYRC 295
Qy 275 LGAVLIIILAGFLAEDWHSRRKRLRHGRAVORPLPPLPQTRKSHG 323
Db 296 YGAY-----NLSSEWSA-----PSDPLDIL-ITGQIHG 322
RESULT 3
I46020
Fc gamma 2 receptor precursor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Accession: I46020; S53115
R;Zhang, G.; Young, J.R.; Tregaskes, C.A.; Sopp, P.; Howard, C.J.
J. Immunol. 155, 1534-1541, 1995
A;Title: Identification of a novel class of mammalian Fc gamma receptor.
A;Reference number: I46020; MUID:95363119; PMID:7636215
A;Accession: I46020
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-264 <ZHA>
A;Cross-references: UNIPROT:Q28109; EMBL:237506; NID:g732571; PIDN:CAA85736.1; PID:g7325
C;Keywords: immunoglobulin receptor
Query Match 23.9%; Score 426.5; DB 2; Length 264;
Best Local Similarity 32.5%; Pred. No. 1e-23;
Matches 112; Conservative 37; Mismatches 87; Indels 109; Gaps 8;
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Qy 1 MSPSPTALFCLGLCLG-RVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRL 59
Db 1 MAPFLPALLCLGLSLGVLRTQVQGTFFKPIIWAEPSSVPLGSSVTILCQGGPNTKFSFL 60
Qy 60 EKLSSS-----RYQDQAVLFIPAMKRSIAGRYCSYQNGSLWSLSQLELVATG- 109
Db 61 NKEGDSFPMNTHPSLEPDWKANFFISNVRBQAGRYCHSHFIGVNWSESPFLDLLVAGE 120
Qy 110 -----VFAKPSLSAQPGAVSSGGDVTLQCTRYGDFQFALYKEG---DPAPYKKNPER-- 159
Db 121 EPAGRLDRPSSLVRPSPGAVNGENVTLCCSGNRTTFLLSKEGAHRPRLRLSQDQDG 180
Qy 160 WYRASFPITITAAHSGTYRCYSFSSRDPYLWSAPSDPLELVVTGTSVTPSRLETPSPSS 219
Db 181 WYQAEFSLSPVTSAGGTTCYRSLSTNPYLLSQSPSEPLALLVAD----- 225
Qy 220 VAEFSEATAELTVSFTNKVFTTTSRITTSKPSDSAPAGRAYTYTKGNLVRLICLGA 279
Db 226 -----YTQNQLIRMGLAASV 240
Qy 280 LIILAGFLAEDWHSRRKRLRHGRAVORPLPPLPQTRKSHG 324
Db 241 LLLL-GIL-----LCQARHDHG 257
RESULT 4
JH0332
Iga (Fc) receptor, myeloid cell (CD89) precursor - human
N;Alternate names: myeloid glycoprotein CD89
C;Species: Homo sapiens (man)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C;Accession: JH0332; I37224; S14405
R;Maliszewski, C.R.; March, C.J.; Schoenborn, M.A.; Gimpel, S.; Shen, L.
J. Exp. Med. 172, 1665-1672, 1990
A;Title: Expression cloning of a human Fc receptor for Iga.
A;Reference number: JH0332; MUID:91079769; PMID:2258698
A;Accession: JH0332
A;Molecule type: mRNA
A;Residues: 1-287 <MAL>
A;Cross-references: UNIPROT:P24071; GB:X54150; NID:g31329; PIDN:CAA38089.1; PID:g31330
A;Experimental source: myeloid cell liver V937
R;de Wit, T.P.; Morton, H.C.; Capel, P.J.; van de Winkel, J.G.
J. Immunol. 155, 1203-1209, 1995
A;Title: Structure of the gene for the human myeloid Iga Fc receptor (CD89).
A;Reference number: I37224; MUID:95363085; PMID:7636188
A;Accession: I37224
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-287 <RES>
A;Cross-references: EMBL:X87767; NID:g963041; PIDN:CAA61039.1; PID:gi054737
C;Genetics:
A;Gene: GDB:FCAR; CD89
A;Cross-references: GDB:127543; OMIM:147045
A;Map position: 19q13.2-19q13.4
A;Introns: 12/1; 24/1; 121/1; 217/1
C;Keywords: glycoprotein; immunoglobulin receptor; transmembrane protein
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-287/Product: Iga receptor Fc alpha #status predicted <MFC>
F;228-246/Domain: transmembrane #status predicted <TRA>
F;65,79,141,177,186/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 21.9%; Score 392; DB 2; Length 287;
Best Local Similarity 33.2%; Pred. No. 3.5e-21;
Matches 100; Conservative 43; Mismatches 110; Indels 68; Gaps 5;
Qy 1 MSPSPTALFCLGLCLG-RVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRL 59
Db 1 MDPKQTTLLCLVLCLGQRIQAEQEGDFMPFISAKSSPVLIDGSKVIQCAIREAYLQTL 60
Qy 60 EKLSSRRYQD-----QAVLFIPAMKRSIAGRYCSYQNGSLWSLSQLELVAT 108
Db 61 MIKNSTYREIGRRLLKFWNETDPEFVIDHMDANKAGRYCQYRIGHYFRYSDTLELVVT 120
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A>Title: Genomic structures and chromosomal location of p91, a novel murine regulatory p  
A:Reference number: JCS894; MUID:98218758; PMID:9538215  
A:Accession: JCS895  
A>Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-680 <VAM>  
A:Cross-references: UNIPROT:O55001; GB:AF041035; NID:g2791691; PIDN:AAB96927.1; PID:g279  
C:Comment: This protein function as inhibitory cell-surface molecule against cell activa  
C:Genetics:  
A:Map position: 7  
F:1-23/Domain: signal sequence #status predicted <SIG>  
F:24-118, 119-220, 221-315, 316-418, 419-517, 518-618/Domain: extracellular Ig-like #status p  
F:636-674/Domain: transmembrane #status predicted <TM>  
F:675-680/Domain: cytoplasmic #status predicted <CYT>  
Query Match 20.0%; Score 356.5; DB 2; Length 680;  
Best Local Similarity 22.9%; Pred. No. 3.6e-18;  
Matches 106; Conservative 50; Mismatches 111; Indels 195; Gaps 7;  
QY 22 SGPSPKPSLQALPSSLVPLEKPVTLRCQGGPPGVLYRLKLSRRYQDAVL----- 73  
DB 220 SGNLQKPTIKAPGSGVITSKRAMTIWCQGNLDAEYVFLHNEKSORTSTOTLQDPGNKR 279  
QY 74 -PIPAKRSLAGRYCSYQNGSLWLSLPDLELVATGVFA--KPSLSAQPGPAVSSGGDV 130  
DB 280 FFIPSTQHAQYRCYCYSSAGNSQPSDTLELVATGIVYNEPRLSLLPSVVRPGNM 339  
QY 131 TLQCQTRYGDFQFALYKEGD-----PAPYKNPERWYRASFPITVTAHSGTYRCYCSFS 184  
DB 340 TLHCASQGHYDKFKLTKEKDFANALDTEHISSSRYQALFIIGTPTTHTGTGTCYGY 399  
QY 185 SRDPYLWASPSDPLELVVTGTSVTS----- 210  
DB 400 KNTPOLWSPVSNLQILISGLSKPSLLTHOGHILDPGWTTLQCFSDMNYDRFALHKVG 459  
QY 211 -----R 211  
DB 460 GADINQHSQQTDIGFSVANFTLVGVSSSTGGQYRCYGAHNLSEWSASSEPLDLITGQ 519  
QY 212 LPTEPPSSV-----AE 222  
DB 520 LPLTSLVQPNHVTGSETVLLCWSMDSVDTFILSKESGAQQPLRLKSKSHDQSQAE 579  
QY 223 FS-----EATAELTVSFTNKVTTTTSRISITSPKES 254  
DB 580 FMSAVTSHLSGTYRCYCAQDSFYLSSASAPVELTVS-----GTIESSSWPPKRP 631  
QY 255 DSPAGPARQYTKGNLVRICLGAVALIILAGFLAEDWHRRK 296  
DB 632 NPPIPTENQDHTMENLRMGAVVVFVLISILATEAWRSRQ 673  
RESULT 9  
G01925  
XLR (cl-11) NK receptor precursor protein - human  
C:Species: Homo sapiens (man)  
C:Date: 21-Dec-1996 #sequence\_revision 06-Jun-1997 #text\_change 09-Jul-2004  
C:Accession: G01925; I61726  
R:Wagtmann, N.  
submitted to the EMBL Data Library, June 1995  
A:Reference number: G08782  
A:Accession: G01925  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-444 <WAG>  
A:Cross-references: UNIPROT:P43629; EMBL:U30274; NID:g1004360; PIDN:AAB52522.1; PID:g100  
R:Colonna, M.; Samaridis, J.  
Science 268, 405-408, 1995  
A>Title: Cloning of immunoglobulin-superfamily members associated with HLA-C and HLA-B  
A:Reference number: A56247; MUID:95232526; PMID:7716543  
A:Accession: I61726  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA

A:Residues: 1-444 <RES>  
A:Cross-references: GB:L41269; NID:g780307; PIDN:AAA69870.1; PID:g780308  
C:Genetics:  
A:Gene: NKAT-3  
A:Map position: 19  
Query Match 18.8%; Score 335; DB 2; Length 444;  
Best Local Similarity 30.4%; Pred. No. 7.8e-17;  
Matches 112; Conservative 34; Mismatches 127; Indels 96; Gaps 12;  
QY 1 MSPSPTALFCLGLCLGRVP-----AOSGGL-----PKPSLQALPSSLVPLEKPV 45  
DB 82 MSPVTTAHAGNYTCRGSHPHSPTGWSAPSNPVIMVTGNHRKPSLLAHGPGPLVKSGERVI 141  
QY 46 LRCQGGPPGVLYRLKLSRRYQDAV-----LFTPAKRSIAGRYRC----- 88  
DB 142 LQCWSDIMFEHFFLHKEGISKDPSRLVGIHDGVSKANFSGPMMALALAGTYRCYGVTH 201  
QY 89 -SYQNGSLWLSLPDLELVATGVFAKPSLSAQPGPAVSSGGDVTLQCOTRYGDFQFALYK 147  
DB 202 TPYQ-----LSAPSDPLDIVVTGPYEKPSLSAQPGKVOAGESVTLSCSSRSYDMYHLSR 257  
QY 148 EGDPAKYNP-----ERWYRASFPITVTAHSGTYRCYCSFSSRDPYLWASPSDPLELV 202  
DB 258 EGGAHERELPAVRKVNRTFQADFPL--GPATHGCTYRCFGSFRHSPIYEMSDPSDPLLVSV 315  
QY 203 TGTSVTSRLPTEPPSSVAEPSEATAELTVSFTNKVTTTTSRISITSPKESDSPAGPAR 262  
DB 316 TG-----NPSSS-----WPSPTBPSSKSGNPR 337  
QY 263 QYTKGNLVRICLGAVALIILAGFLAEDWHRRKLRHRAVQRPPLPPLPQTRKSH 322  
DB 338 HLHI-----LIGTSVVIILFILLFLLHLCWCSNKK-----NAAV-----MQOEPAGNRKA 383  
QY 323 GQDQGGROD 331  
DB 384 NSEDSDEQD 392  
RESULT 10  
B53434  
cell surface glycoprotein gp49B form 2 precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 19-May-1995 #sequence\_revision 19-May-1995 #text\_change 09-Jul-2004  
C:Accession: B53434  
R:Castells, M.C.; Wu, X.; Akm, J.P.; Austen, K.F.; Katz, H.R.  
J. Biol. Chem. 269, 8393-8401, 1994  
A>Title: Cloning of the gp49B gene of the immunoglobulin superfamily and demonstration th  
A:Reference number: A53434; MUID:94179223; PMID:8132564  
A:Accession: B53434  
A>Status: preliminary  
A:Molecule type: DNA; mRNA  
A:Residues: 1-296 <CAS>  
A:Cross-references: UNIPROT:Q64281; GB:U05265; NID:g475446; PIDN:AAAL7798.1; PID:g475448;  
C:Genetics:  
A:Gene: gp49B  
A:Introns: 12/3; 24/2; 119/2; 220/1; 232/1; 249/3; 272/1  
C:Keywords: alternative splicing; glycoprotein  
Query Match 18.5%; Score 330; DB 2; Length 296;  
Best Local Similarity 36.1%; Pred. No. 1.1e-16;  
Matches 88; Conservative 33; Mismatches 101; Indels 22; Gaps 6;  
QY 6 TALFCLGLCL-GRVPAOSGGLPKPSLQALPSSLVPLEKPVTLRCQGGPVGVLYRLKLS 64  
DB 6 TVLLYGLILEPRTAVOAGHLPKPIIWAEPGSVIAAYTSVITWCQGSWEAQYVHYLKEKS 65  
QY 65 SRYQD-----QAVLFIPAMKRSLAGRYCSYQNGSLWLSLPDLELVATGVFAKPS 115  
DB 66 VNPWDTQVPLETRNKAKNPIFSMTTSYAGIYKCYESAAGFSEHSDAMELVMTGAYENPS 125  
QY 116 LSAQPGPAVSSGGDVTLQCOTRYGDFQFALYKEG-----DPAPYKNPERWYRASFP 167

Db 126 LSVYSSNVTSGVSISSFCSSSIVFCRFLIQEGKHLSTWLDLSDHQANQPSY--ATFVL 183  
Qy 168 ITVTAHSGTYRCYCFSSRDPLMSAPSDPLBLVVTGTSVTPSRLPTEPPSSVAEF-SEA 226  
Db 184 DAVTPNHNGTFRCYGFRNEPQWSPKSNLDMISETK-DQSSPTPTDASVKNQTSN 242  
Qy 227 TAEI 230  
Db 243 NAEI 246

RESULT 11  
A56247  
natural killer cell-associated protein - human  
C:Species: Homo sapiens (man)  
C:Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 09-Jul-2004  
R:Colonna, M.; Samaridis, J.  
Science 268, 405-408, 1995  
A:Title: Cloning of immunoglobulin-superfamily members associated with HLA-C and HLA-B  
A:Reference number: A56247; MUID:95232526; PMID:7716543  
A:Accession: A56247  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-348 <RES>  
A:Cross-references: UNIPROT:P43626; GB:L41267; NID:G780303; PIDN:AAA69869.1; PID:G780304  
C:Genetics:  
A:Gene: GDB:NKAT1  
A:Cross-references: GDB:698165  
A:Map position: 19

Query Match 18.4%; Score 328; DB 2; Length 348;  
Best Local Similarity 31.0%; Pred. No. 1.9e-16;  
Matches 101; Conservative 34; Mismatches 107; Indels 84; Gaps 11;

Qy 1 MSPSPALFCLGLCL--GRVPAQSGPLPKPSLQALPSSLVPLEKPYTLRCQGGVLDLYR 58  
Db 1 MSLLVSMACVGFLLQGWHP-HEGVHRKPSLLAHGPGVLEKSEETVILQCSWDVMEHFL 59  
Qy 59 LEKLSSRYQD-----QAVLFIAMKRSAGRYRC-----SYQNGSLWSL 98  
Db 60 LHR--EGMENDTLRLGEGHGDGSKANFSIRMTQDLAGTYRCYGVSVTHSPYQ----VSA 113  
Qy 99 PSDQLVATGVFAKPSLAQPGVSSGGDVTLCQTRYGDFQFALYKEGDPAPYKNP- 157  
Db 114 PSDPLDIVIIGLYKEPSLAQPGTVLAGENVTLSCSSRSYDMVHLSREGEAHERRLPA 173  
Qy 158 -----ERWYRASPIITVTAHSGTYRCYCFSSRDPLMSAPSDPLBLVVTGTSVTPSRLP 213  
Db 174 GPKVNGTFQADFP--GPATHGTYRCFGSHDPSYKSDPLLLSVTGNPSNWSPP 231  
Qy 214 TEPPSSVAEFSEATAELTVSTNKVTTTTSRITTSKESDPSAGPARQYVYTKGNLVRI 273  
Db 232 TEPSK-----TGPRH-----LHI 246  
Qy 274 CLG---AVILILAGLAEDWHSRRK 296  
Db 247 LGTGSVVIILFILLFLLHRCWCSNKK 272

RESULT 12  
G01924  
KIR (cl-2) NK receptor precursor - human  
N:Alternate names: killer cell inhibitory receptor  
C:Species: Homo sapiens (man)  
C:Date: 21-Dec-1996 #sequence\_revision 06-Jun-1997 #text\_change 05-Nov-1999  
C:Accession: G01924; G01945  
R:Wagtmann, N.  
submitted to the EMBL Data Library, June 1995  
A:Reference number: G08780  
A:Accession: G01924  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA

A:Residues: 1-444 <WAG>  
A:Cross-references: EMBL:U30273; NID:G1004358; PIDN:AAAS2521.1; PID:G1004359  
R:D'Andrea, A.; Chang, C.; Franz-Bacon, K.; McClanahan, T.; Phillips, J.H.; Lanier, L.L.  
submitted to the EMBL Data Library, July 1995  
A:Reference number: G08908  
A:Accession: G01945  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-444 <DXA>  
A:Cross-references: EMBL:U31416; NID:G973405; PIDN:AAC23725.1; PID:G973406  
C:Genetics:  
A:Gene: NKBI

Query Match 18.3%; Score 327; DB 2; Length 444;  
Best Local Similarity 30.1%; Pred. No. 2.9e-16;  
Matches 111; Conservative 34; Mismatches 128; Indels 96; Gaps 12;

Qy 1 MSPSPALFCLGLCLGRVP-----AOSGPI-----PKPSLQALPSSLVPLEKPYT 45  
Db 82 MSPVTTAHAGNYTCRSHPSPTGWSAPSNPVIVTGNHRKPSLLAHGPGVLEKSERVI 141  
Qy 46 LRCQGGVLDLYRLEKLSRRYQDAV-----LFIAMKRSAGRYRC-----88  
Db 142 LQCSWDIMFEHFLHKEGISKDPSRLVGQIHGVSKANFSIGPMMLALAGTYRCYGVSVTH 201  
Qy 89 -SYQNGSLWSLPSDQLELVATGVFAKPSLAQPGVSSGGDVTLCQTRYGDFQFALYK 147  
Db 202 TPTYQ-----LSAFSDPLDIVVTGYEKPSSLAQPGVQAGESVTLSCSSRSYDMVHLSR 257  
Qy 148 EGDPAPIKNP-----ERWYRASPIITVTAHSGTYRCYCFSSRDPLMSAPSDPLLELV 202  
Db 258 ERGAHERRLPAVKVNRTFQADFP--GPATHGTYRCFGSHPSYKSDPSDPLLVSV 315  
Qy 203 TCTSVPTRSLTEPPSSVAEFSEATAELTVSTNKVTTTTSRITTSKESDPSAGPAR 262  
Db 316 TG-----NPSSS-----WPSPTSPSSKSGNPR 337  
Qy 263 QYTKGNLVIRICLGAIVILLAGLAEDWHSRRKRLHRGRAVQRPPLPPLPQTRKSH 322  
Db 338 LHUI---LIGTSVVIILFILLFLLHRCWCSNKK-----NAAV-----WQSPAGNRTA 383  
Qy 323 GGQDGGROD 331  
Db 384 NSEDSDEQD 392

RESULT 13  
I61725  
natural killer associated transcript 2 - human  
C:Species: Homo sapiens (man)  
C:Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 09-Jul-2004  
C:Accession: I61725  
R:Colonna, M.; Samaridis, J.  
Science 268, 405-408, 1995  
A:Title: Cloning of immunoglobulin-superfamily members associated with HLA-C and HLA-B  
A:Reference number: A56247; MUID:95232526; PMID:7716543  
A:Accession: I61725  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-341 <RES>  
A:Cross-references: UNIPROT:P43628; GB:L41268; NID:G780305; PIDN:AAA69869.1; PID:G780306  
C:Genetics:  
A:Gene: NKAT-2

Query Match 18.1%; Score 323.5; DB 2; Length 341;  
Best Local Similarity 30.1%; Pred. No. 3.9e-16;  
Matches 99; Conservative 36; Mismatches 105; Indels 89; Gaps 12;

Qy 1 MSPSPALFCLGLCL--GRVPAQSGPLPKPSLQALPSSLVPLEKPYTLRCQGGVLDLYR 58  
Db 1 MSLLVSMVGVGFLLQGWHP-HEGVHRKPSLLAHGPGVLEKSEETVILQCSWDVMEHFL 59  
Qy 59 LEKLSSRYQD-----QAVLFIAMKRSAGRYRC-----SYQNGSLWSL 98

Db 60 LHR--EGFKDTLHLIGHBHGVSKANFSIGPMQDLAGTYRCVGSVTHSYQ-----LSA 113  
Qy 99 PSDQLVLVATGVFAKPSLSAQPGPAVSSGGDVTLQCQTRYGDFQFALYKEGD-----P 151  
Db 114 PSDPLDIVITGLYKPSLSAQPGPTVLAGESTVTLSCSSRSYDMVHLGREGEAHERRPSA 173  
Qy 152 APYKNPERWYRASPIITVTAHSGTYRCYFSRSDPYLWSAPSDPLELVVTGTSVTPSR 211  
Db 174 GPKVNGT--FOADPFL--GPATHGGTYRCFGSRDPSYEWNSSDPLLVSVTGNPSNSWP 229  
Qy 212 LPTEPPSSVAEFSSEATBLTVSFNTKVTFTTSRITTSKESDPSGAPARQYVTKGNLV 271  
Db 230 SPTEPSE-----TGNPRH-----L 244  
Qy 272 RICLGA-----VILIILAGFLAEDWHSRRK 296  
Db 245 HVLIGTSVVIIIFILLFFLLHRMCCNK 273  
RESULT 14  
T09402  
immunoglobulin-like protein IGSF1 - human  
C:Species: Homo sapiens (man)  
C>Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
C:Accession: T09402  
R:Mazzarella, R.; Pengue, G.; Jones, J.; Jones, C.; Schlessinger, D.  
Genomics 48, 157-162, 1998  
A:Title: Cloning and expression of an immunoglobulin superfamily gene (IGSF1) in Xq25.  
A:Reference number: Z16665; MUID:98190514; PMID:9521868  
A:Accession: T09402  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-1327 <MAZ>  
A:Cross-references: UNIPROT:O15070; EMBL:AF034198; NID:g2645889; PIDN:AACS2057.1; PID:g2  
C:Genetics:  
A:Gene: Igsf1  
A:Map position: Xq25

Query Match 18.0%; Score 322; DB 2; Length 1327;  
Best Local Similarity 32.1%; Pred. No. 2.5e-15;  
Matches 105; Conservative 37; Mismatches 133; Indels 52; Gaps 9;  
Qy 26 PKPSIQALPSSLVPLEKPVTLRCQGP---PGVDLYRLEKLSRRY-----QDQAVLFIPAM 78  
Db 960 PKPWLFAEPSSVPMGQNVTLRCRFGVHGVIYHKEGEATSMQLWGTSNDGAPPIITNI 1019  
Qy 79 KESLAGRYRCSYQ---NGSLWSLPSDQLVLVATGVFAKPSLSAQPGPAVSSGGDVTLQCQ 135  
Db 1020 SGTSMGRYSCCVHPDWTSSIKIQPSNTLELVTLGLPRLPSLLAQPGPMVAPGENWTLQCQ 1079  
Qy 136 TRYGDFQFALYKEG--DPAPYKNPERWYRASPIITVTAHSGTYRCYFSRSDPYLWSA 193  
Db 1080 GELPDSTFVLLKEGAQEPLEQQRPS--GYRADPMPAVRGEDSGIYSCVYILDSTPFAASN 1138  
Qy 194 PSDPLELVVTGTSVTPS-----RLTEPPSSVAEP-----SEATAELT- 231  
Db 1139 HSDSLEIWTDPKPKPSLSAMPSTWFKLGKDITLQCRGLPGVEFVLEHDEGEAPQPFSE 1198  
Qy 232 -----VSFTNKVFTTTSRITTSKESDPSGAPARQYVTKGNLVRLCL 275  
Db 1199 DGDFFVNNVEGKIGNYCSYRLQAYPIWSPSPDLELVGAAGPVAQECTVGNIVRSLSL 1258  
Qy 276 GAVILIILAGFLAEDWHSRRKRLHRG 302  
Db 1259 IVVVVVLGVLAIEW-KKWPLRLTRG 1284

RESULT 15  
A53434  
cell surface glycoprotein gp49B form 1 precursor - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 19-May-1995 #sequence\_revision 19-May-1995 #text\_change 09-Jul-2004

C:Accession: A53434  
R:Castells, M.C.; Wu, X.; Arm, J.P.; Austen, K.P.; Katz, H.R.  
J. Biol. Chem. 269, 8393-8401, 1994  
A:Title: Cloning of the gp49B gene of the immunoglobulin superfamily and demonstration th  
A:Reference number: A53434; MUID:94119223; PMID:8132564  
A:Accession: A53434  
A:Status: preliminary  
A:Molecule type: DNA; mRNA  
A:Residues: 1-335 <CAS>  
A:Cross-references: UNIPROT:Q64281; GB:U05265; NID:g475446; PIDN:AAA17797.1; PID:g475447;  
C:Genetics:  
A:Gene: Gp49B  
A:Introns: 12/3; 24/2; 119/2; 220/1; 232/1; 271/1; 288/3; 311/1  
C:Keywords: alternative splicing; glycoprotein  
Query Match 17.8%; Score 317.5; DB 2; Length 335;  
Best Local Similarity 34.0%; Pred. No. 1e-15;  
Matches 84; Conservative 36; Mismatches 104; Indels 23; Gaps 6;  
Qy 6 TALECLGLCL-GRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPVGVLDYRLEKLS 64  
Db 6 TVLLYLGLIILEPRTPAVQAGHLPKFIWAEPGSGVIAATSVITWCQGSWEAQYHYLYKEKS 65  
Qy 65 SRYQD-----QAVLFIPAMKRSLAGRYRCSYQNGSLWSLPSDQLVLVATGVFAKPS 115  
Db 66 VNPMDTQVPLETRNKAKFNIPSMTTSYAGIYKYESAAGFSEHSDAMELVMTGAYENPS 125  
Qy 116 LSAQPGPAVSSGGDVTLQCQTRYGDFQFALYKEG-----DPAPYKNPERWYRASPII 167  
Db 126 LSVYPPSSNVITSGVISISFSCSSSIVFGRFILLIQEGKGLSWTLDSQHQANQPSY--ATPVL 183  
Qy 168 ITVTAHSGTYRCYFSRSDPYLWSAPSDPLELVVTGTSVTPSRLPTEPPSSVAEFSSEAT 227  
Db 184 DAVTPNHNGTRFCYGRFNEPQVWSPKPSNSLDLMISETK-DQSSTPTB--DGLEYQKIL 240  
Qy 228 AELTVSF 234  
Db 241 IGVLVSP 247

Search completed: October 29, 2005, 02:57:49  
Job time : 42 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 29, 2005, 03:38:13 ; Search time 41 Seconds

(without alignments)  
453.357 Million cell updates/sec

Title: US-09-503-387-3\_COPY\_21\_269

Perfect score: 1304

Sequence: 1 QSGPLPRLPSLQALPSSLVPL.....SPKESDSPAGPARQYTKGN 249

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 413575

Minimum DB seq length: 0

Maximum DB seq length: 250

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/ptodata/1/iaa/5A COMB.pap:\*

2: /cgn2\_6/ptodata/1/iaa/5B COMB.pap:\*

3: /cgn2\_6/ptodata/1/iaa/6A COMB.pap:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1304	100.0	249	3	US-09-345-468-9
2	1304	100.0	249	3	US-09-414-453A-9
3	268	20.6	47	3	US-09-345-468-7
4	268	20.6	47	3	US-09-414-453A-7
5	220	16.9	47	3	US-09-345-468-23
6	220	16.9	47	3	US-09-414-453A-23
7	216	16.6	41	3	US-09-345-468-6
8	216	16.6	41	3	US-09-414-453A-6
9	187	14.3	50	3	US-09-345-468-13
10	187	14.3	50	3	US-09-414-453A-13
11	164	12.6	41	3	US-09-345-468-22
12	164	12.6	41	3	US-09-414-453A-22
13	162.5	12.5	135	3	US-08-985-950-10
14	162.5	12.5	135	4	US-09-546-049-10
15	131	10.0	105	4	US-09-513-999C-4313
16	100	7.7	172	2	US-08-756-387B-13
17	100	7.7	172	3	US-09-285-873-13
18	100	7.7	172	4	US-09-245-764-9
19	100	7.7	172	4	US-09-944-277A-13
20	100	7.7	197	2	US-08-756-387B-11
21	100	7.7	197	3	US-09-285-873-11
22	100	7.7	197	4	US-09-944-277A-11
23	100	7.7	232	1	US-07-869-933-13
24	100	7.7	232	2	US-08-756-387B-6
25	100	7.7	232	3	US-09-103-663-13
26	100	7.7	232	3	US-09-285-873-6
27	100	7.7	232	4	US-09-944-277A-6

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Patent No. 5169835  
Sequence 219, App  
Sequence 145, App  
Sequence 215, App  
Sequence 141, App  
Sequence 22, App

ALIGNMENTS

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RESULT 1
US-09-345-468-9
; Sequence 9, Application US/09345468
; Patent No. 6245527
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Villevall, J.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-147
; CURRENT APPLICATION NUMBER: US/09/345,468
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-345-468-9

Query Match      100.0%; Score 1304; DB 3; Length 249;
Best Local Similarity 100.0%; Pred. No. 6.6e-121;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRLEKLSRRYQDOAVLFIPAMKR 60
Db 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRLEKLSRRYQDOAVLFIPAMKR 60

Qy 61 SLAGRYCSYONGSLMSLPDQLVLVATGVFAKPSLSAQPGPAVSSGGDVTLCQTRYGF 120
Db 61 SLAGRYCSYONGSLMSLPDQLVLVATGVFAKPSLSAQPGPAVSSGGDVTLCQTRYGF 120

Qy 121 DQFALYKEGDPAPYKNPERWYRASFPFIITVTAHSGTYRCYFSFSSRDPYLWSAPSDPLEL 180
Db 121 DQFALYKEGDPAPYKNPERWYRASFPFIITVTAHSGTYRCYFSFSSRDPYLWSAPSDPLEL 180

Qy 181 VVTGTSVTPSRLPTEPPSSVAEFSEATAELTVSTNKFVTTTTSRSTTSKESDSPAGP 240
Db 181 VVTGTSVTPSRLPTEPPSSVAEFSEATAELTVSTNKFVTTTTSRSTTSKESDSPAGP 240

Qy 241 ARQYTTKGN 249
Db 241 ARQYTTKGN 249

RESULT 2
US-09-414-453A-9
; Sequence 9, Application US/09414453A
; Patent No. 6383779
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Villevall, J.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-147
; CURRENT APPLICATION NUMBER: US/09/414,453A
; CURRENT FILING DATE: 1999-10-07
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-414-453A-9

Query Match      100.0%; Score 1304; DB 3; Length 249;
Best Local Similarity 100.0%; Pred. No. 6.6e-121;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRLEKLSRRYQDOAVLFIPAMKR 60
Db 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRLEKLSRRYQDOAVLFIPAMKR 60

Qy 61 SLAGRYCSYONGSLMSLPDQLVLVATGVFAKPSLSAQPGPAVSSGGDVTLCQTRYGF 120
Db 61 SLAGRYCSYONGSLMSLPDQLVLVATGVFAKPSLSAQPGPAVSSGGDVTLCQTRYGF 120

Qy 121 DQFALYKEGDPAPYKNPERWYRASFPFIITVTAHSGTYRCYFSFSSRDPYLWSAPSDPLEL 180
Db 121 DQFALYKEGDPAPYKNPERWYRASFPFIITVTAHSGTYRCYFSFSSRDPYLWSAPSDPLEL 180

Qy 181 VVTGTSVTPSRLPTEPPSSVAEFSEATAELTVSTNKFVTTTTSRSTTSKESDSPAGP 240
Db 181 VVTGTSVTPSRLPTEPPSSVAEFSEATAELTVSTNKFVTTTTSRSTTSKESDSPAGP 240

Qy 241 ARQYTTKGN 249
Db 241 ARQYTTKGN 249

RESULT 3
US-09-345-468-7
; Sequence 7, Application US/09345468
; Patent No. 6245527
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Villevall, J.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-147
; CURRENT APPLICATION NUMBER: US/09/345,468
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-345-468-7

Query Match      20.6%; Score 268; DB 3; Length 47;
Best Local Similarity 100.0%; Pred. No. 1.8e-19;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 114 CQTRYGFDQFALYKEGDPAPYKNPERWYRASFPFIITVTAHSGTYRC 160
Db 1 CQTRYGFDQFALYKEGDPAPYKNPERWYRASFPFIITVTAHSGTYRC 47

RESULT 4
US-09-414-453A-7
; Sequence 7, Application US/09414453A
; Patent No. 6383779
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Villevall, J.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-147
; CURRENT APPLICATION NUMBER: US/09/414,453A
; CURRENT FILING DATE: 1999-10-07
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-414-453A-7
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Query Match      100.0%; Score 1304; DB 3; Length 249;
Best Local Similarity 100.0%; Pred. No. 6.6e-121;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRLEKLSRRYQDOAVLFIPAMKR 60
Db 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRLEKLSRRYQDOAVLFIPAMKR 60

Qy 61 SLAGRYCSYONGSLMSLPDQLVLVATGVFAKPSLSAQPGPAVSSGGDVTLCQTRYGF 120
Db 61 SLAGRYCSYONGSLMSLPDQLVLVATGVFAKPSLSAQPGPAVSSGGDVTLCQTRYGF 120

Qy 121 DQFALYKEGDPAPYKNPERWYRASFPFIITVTAHSGTYRCYFSFSSRDPYLWSAPSDPLEL 180
Db 121 DQFALYKEGDPAPYKNPERWYRASFPFIITVTAHSGTYRCYFSFSSRDPYLWSAPSDPLEL 180

Qy 181 VVTGTSVTPSRLPTEPPSSVAEFSEATAELTVSTNKFVTTTTSRSTTSKESDSPAGP 240
Db 181 VVTGTSVTPSRLPTEPPSSVAEFSEATAELTVSTNKFVTTTTSRSTTSKESDSPAGP 240

Qy 241 ARQYTTKGN 249
Db 241 ARQYTTKGN 249

RESULT 3
US-09-345-468-7
; Sequence 7, Application US/09345468
; Patent No. 6245527
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Villevall, J.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-147
; CURRENT APPLICATION NUMBER: US/09/345,468
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-345-468-7

Query Match      20.6%; Score 268; DB 3; Length 47;
Best Local Similarity 100.0%; Pred. No. 1.8e-19;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 114 CQTRYGFDQFALYKEGDPAPYKNPERWYRASFPFIITVTAHSGTYRC 160
Db 1 CQTRYGFDQFALYKEGDPAPYKNPERWYRASFPFIITVTAHSGTYRC 47

RESULT 4
US-09-414-453A-7
; Sequence 7, Application US/09414453A
; Patent No. 6383779
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Villevall, J.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-147
; CURRENT APPLICATION NUMBER: US/09/414,453A
; CURRENT FILING DATE: 1999-10-07
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-414-453A-7
```



```

; SEQ ID NO 7
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-414-453A-7

Query Match      20.6%; Score 268; DB 3; Length 47;
Best Local Similarity 100.0%; Pred. No. 1.8e-19;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 114 CQTRYGDFQFALYKGGDPAPYKNPWRWYRASFPFIITVTAHSGTYRC 160
Db 1 CQTRYGDFQFALYKGGDPAPYKNPWRWYRASFPFIITVTAHSGTYRC 47

RESULT 5
US-09-345-468-23
; Sequence 23, Application US/09345468
; Patent No. 6245527
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Villevall, J.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-147
; CURRENT APPLICATION NUMBER: US/09/345,468
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-345-468-23

Query Match      16.9%; Score 220; DB 3; Length 47;
Best Local Similarity 78.7%; Pred. No. 1e-14;
Matches 37; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 114 CQTRYGDFQFALYKGGDPAPYKNPWRWYRASFPFIITVTAHSGTYRC 160
Db 1 CQSPYSFDFVLYKGGDTGPKRPEKWKYRANFPFIITVTAHSGTYRC 47

RESULT 6
US-09-414-453A-23
; Sequence 23, Application US/09414453A
; Patent No. 6383779
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Villevall, J.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-147
; CURRENT APPLICATION NUMBER: US/09/414,453A
; CURRENT FILING DATE: 1999-10-07
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-414-453A-23

Query Match      16.9%; Score 220; DB 3; Length 47;
Best Local Similarity 78.7%; Pred. No. 1e-14;
Matches 37; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 114 CQTRYGDFQFALYKGGDPAPYKNPWRWYRASFPFIITVTAHSGTYRC 160
Db 1 CQSPYSFDFVLYKGGDTGPKRPEKWKYRANFPFIITVTAHSGTYRC 47

RESULT 7
US-09-345-468-6
; Sequence 6, Application US/09345468
; Patent No. 6245527
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Villevall, J.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-147
; CURRENT APPLICATION NUMBER: US/09/345,468
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-345-468-6

Query Match      16.6%; Score 216; DB 3; Length 41;
Best Local Similarity 100.0%; Pred. No. 2.1e-14;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 CQPPGVDLYRLEKLSRSSRYODQAVLFIPAMKRSIAGRYRC 68
Db 1 CQPPGVDLYRLEKLSRSSRYODQAVLFIPAMKRSIAGRYRC 41

RESULT 8
US-09-414-453A-6
; Sequence 6, Application US/09414453A
; Patent No. 6383779
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Villevall, J.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-147
; CURRENT APPLICATION NUMBER: US/09/414,453A
; CURRENT FILING DATE: 1999-10-07
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-414-453A-6

Query Match      16.6%; Score 216; DB 3; Length 41;
Best Local Similarity 100.0%; Pred. No. 2.1e-14;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 CQPPGVDLYRLEKLSRSSRYODQAVLFIPAMKRSIAGRYRC 68
Db 1 CQPPGVDLYRLEKLSRSSRYODQAVLFIPAMKRSIAGRYRC 41

RESULT 9
US-09-345-468-13
; Sequence 13, Application US/09345468
; Patent No. 6245527
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Villevall, J.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-147
; CURRENT APPLICATION NUMBER: US/09/345,468
; CURRENT FILING DATE: 1999-10-07
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-345-468-13

Query Match      16.9%; Score 220; DB 3; Length 47;
Best Local Similarity 78.7%; Pred. No. 1e-14;
Matches 37; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 114 CQTRYGDFQFALYKGGDPAPYKNPWRWYRASFPFIITVTAHSGTYRC 160
Db 1 CQTRYGDFQFALYKGGDPAPYKNPWRWYRASFPFIITVTAHSGTYRC 47
```

```
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Vaichenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-147
; CURRENT APPLICATION NUMBER: US/09/345,468
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-345-468-13

Query Match      14.3%; Score 187; DB 3; Length 50;
Best Local Similarity 74.5%; Pred. No. 2e-11;
Matches 35; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Qy 24 VTLRCQPPGVLDYLRLEKLSRRYQDQAVLFIPAMKSLAGRYCSY 70
Db 4 VILRCQPPDVLRLKLEKPKYEDQDFLFIPTMERSNAGRYCSY 50

RESULT 10
US-09-414-453A-13
; Sequence 13, Application US/09414453A
; Patent No. 6383779
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Villevall, J.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Vaichenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-147
; CURRENT APPLICATION NUMBER: US/09/414,453A
; CURRENT FILING DATE: 1999-10-07
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-414-453A-13

Query Match      14.3%; Score 187; DB 3; Length 50;
Best Local Similarity 74.5%; Pred. No. 2e-11;
Matches 35; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Qy 24 VTLRCQPPGVLDYLRLEKLSRRYQDQAVLFIPAMKSLAGRYCSY 70
Db 4 VILRCQPPDVLRLKLEKPKYEDQDFLFIPTMERSNAGRYCSY 50

RESULT 11
US-09-345-468-22
; Sequence 22, Application US/09345468
; Patent No. 6245527
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Villevall, J.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Vaichenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-147
; CURRENT APPLICATION NUMBER: US/09/345,468
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 41
; TYPE: PRT
```

```
; ORGANISM: Mus musculus
US-09-345-468-22

Query Match      12.6%; Score 164; DB 3; Length 41;
Best Local Similarity 73.2%; Pred. No. 2.9e-09;
Matches 30; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 28 CQPPGVLDYLRLEKLSRRYQDQAVLFIPAMKSLAGRYC 68
Db 1 CQPPDVLRLKLEKPKYEDQDFLFIPTMERSNAGRYC 41

RESULT 12
US-09-414-453A-22
; Sequence 22, Application US/09414453A
; Patent No. 6383779
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Villevall, J.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Vaichenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-147
; CURRENT APPLICATION NUMBER: US/09/414,453A
; CURRENT FILING DATE: 1999-10-07
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-414-453A-22

Query Match      12.6%; Score 164; DB 3; Length 41;
Best Local Similarity 73.2%; Pred. No. 2.9e-09;
Matches 30; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 28 CQPPGVLDYLRLEKLSRRYQDQAVLFIPAMKSLAGRYC 68
Db 1 CQPPDVLRLKLEKPKYEDQDFLFIPTMERSNAGRYC 41

RESULT 13
US-08-985-950-10
; Sequence 10, Application US/08985950
; Patent No. 6140076
; GENERAL INFORMATION:
; APPLICANT: Adema, Gosse Jan
; TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,950
; FILING DATE: 05-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/041,279
; FILING DATE: 21-MARCH-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/033,181
```

FILING DATE: 16-DEC-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/032,252  
FILING DATE: 06-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0670K  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650)852-9196  
TELEFAX: (650)496-1204  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 135 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-985-950-10

Query Match 12.5%; Score 162.5; DB 3; Length 135;  
Best Local Similarity 31.6%; Pred. No. 2.3e-08;  
Matches 42; Conservative 15; Mismatches 43; Indels 33; Gaps 3;

QY 1 QSGPLPKPSLQALPSSLPVLEKPVTLRCQGGPPGVLDYLRLEKLSRRYQD----- 49  
DB 22 QEGALPRPSISAEPGTIVSPGSHVTFMCRGPGVGVQTFRLEREDRAKYKDSYNVFRLGPE 81

QY 50 -QAVLFIPAMKRSAGRYCSYQNGSLWSPDQLELVATGVFAKPSLSAOPGPAVSSGG 108  
DB 82 SEARFHDSVSEGNAGLYRCLYKPPGWSHSDFLLELVKGT-----PGTEAS--- 130

QY 109 DVTLCQCTRYGFD 121  
DB 131 -----GFD 133

RESULT 14  
US-09-546-049-10  
Sequence 10, Application US/09546049  
Patent No. 6479638  
GENERAL INFORMATION:  
APPLICANT: Adema, Gosse Jan  
Meygaard, Linde  
Gorman, Daniel M.  
McClanahan, Terrill K.  
Zurawski, Sandra M.  
Lanier, Lewis L.  
Phillips Jr., Joseph H.  
TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;  
Related Reagents  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESS: DNAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/546,049  
FILING DATE: 10-Apr-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/985,950  
FILING DATE: 05-DEC-1997  
APPLICATION NUMBER: US 60/041,279  
FILING DATE: 21-MARCH-1997  
APPLICATION NUMBER: US 60/033,181

FILING DATE: 16-DEC-1996  
APPLICATION NUMBER: US 60/032,252  
FILING DATE: 06-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0670K  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650)852-9196  
TELEFAX: (650)496-1204  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 135 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
US-09-546-049-10

Query Match 12.5%; Score 162.5; DB 4; Length 135;  
Best Local Similarity 31.6%; Pred. No. 2.3e-08;  
Matches 42; Conservative 15; Mismatches 43; Indels 33; Gaps 3;

QY 1 QSGPLPKPSLQALPSSLPVLEKPVTLRCQGGPPGVLDYLRLEKLSRRYQD----- 49  
DB 22 QEGALPRPSISAEPGTIVSPGSHVTFMCRGPGVGVQTFRLEREDRAKYKDSYNVFRLGPE 81

QY 50 -QAVLFIPAMKRSAGRYCSYQNGSLWSPDQLELVATGVFAKPSLSAOPGPAVSSGG 108  
DB 82 SEARFHDSVSEGNAGLYRCLYKPPGWSHSDFLLELVKGT-----PGTEAS--- 130

QY 109 DVTLCQCTRYGFD 121  
DB 131 -----GFD 133

RESULT 15  
US-09-513-999C-4313  
Sequence 4313, Application US/09513999C  
Patent No. 6783961  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Duclert, A.  
APPLICANT: Giordano, J.Y.  
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
Patent No. 6783961  
FILE REFERENCE: 59.US2.REG  
CURRENT APPLICATION NUMBER: US/09/513.999C  
CURRENT FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/122,487  
PRIOR FILING DATE: 1999-02-26  
NUMBER OF SEQ ID NOS: 36681  
SEQ ID NO 4313  
LENGTH: 105  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SIGNAL  
LOCATION: -21...-1  
OTHER INFORMATION: score 9.5  
OTHER INFORMATION: seq LGLVLCLAQTIHT/QE  
FEATURE:  
NAME/KEY: UNSURE  
LOCATION: 47  
OTHER INFORMATION: Xaa= \* or Tyr  
US-09-513-999C-4313

Query Match 10.0%; Score 131; DB 4; Length 105;  
Best Local Similarity 36.6%; Pred. No. 2.1e-05;  
Matches 30; Conservative 11; Mismatches 29; Indels 12; Gaps 1;

QY 1 QSGPLPKPSLQALPSSLPVLEKPVTLRCQGGPPGVLDYLRLEKLSRRYQD----- 49

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Db 22 QEEELPPRSIAEGTGVIPLGSHVTVCRGPGVGVQVTFRLERESRSTXNDTSDVSQASPSE 81
Qy 50 -QAVLFIPAMKRSIAGRYCSY 70
Db 82 SEARFRIDSVSEGNAGPYRCIY 103

RESULT 16
US-08-756-387B-13
; Sequence 13, Application US/08756387B
; Patent No. 5945294
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heeka Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; FILING DATE: No. 5945294ember 26, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 172 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-756-387B-13

Query Match 7.7%; Score 100; DB 2; Length 172;
Best Local Similarity 24.7%; Pred. No. 0.049;
Matches 47; Conservative 27; Mismatches 78; Indels 38; Gaps 9;

Qy 6 PKPSLQALPSSLVPLEKPVTLRCQPGPVLDYRLKLSRSRY-----QDQAVLFIPA 57
Db 5 PKVSLNP-PWNRIFKGENVTLCNG-----NNFEVSVSTKWFHNGSLSEETNSSLNIVN 57
Qy 58 MKRSIAGRYCSYONGSLWSPDLQELVATGVFAKPSLSAQPGPAYSSGGDVTLCQOTR 117
Db 58 AKFEDSEYKCOHQ-----VNESEPVYLEVFSDWLLLOQASAEVVMGQPLFLRCHGW 110
Qy 118 YGFDQFAL--YKEGDPAPYKNPERWY-RASFPITVTAAHSGTYRCYSFSSRDPYLWSA- 173
Db 111 RNWDVYKVIYKDGKALKY-----WYENHNISITNATVEDSGTYCTG-----KWQLD 159
Qy 174 -PSDPLELV 182
Db 160 YESEPLNITV 169

RESULT 17
US-09-285-873-13
; Sequence 13, Application US/09285873
; Patent No. 6309832
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heeka Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; FILING DATE: US/09/285,873
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387
; FILING DATE: No. 6309832ember 26, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 172 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-285-873-13

Query Match 7.7%; Score 100; DB 3; Length 172;
Best Local Similarity 24.7%; Pred. No. 0.049;
Matches 47; Conservative 27; Mismatches 78; Indels 38; Gaps 9;

Qy 6 PKPSLQALPSSLVPLEKPVTLRCQPGPVLDYRLKLSRSRY-----QDQAVLFIPA 57
Db 5 PKVSLNP-PWNRIFKGENVTLCNG-----NNFEVSVSTKWFHNGSLSEETNSSLNIVN 57
Qy 58 MKRSIAGRYCSYONGSLWSPDLQELVATGVFAKPSLSAQPGPAYSSGGDVTLCQOTR 117
Db 58 AKFEDSEYKCOHQ-----VNESEPVYLEVFSDWLLLOQASAEVVMGQPLFLRCHGW 110
Qy 118 YGFDQFAL--YKEGDPAPYKNPERWY-RASFPITVTAAHSGTYRCYSFSSRDPYLWSA- 173
Db 111 RNWDVYKVIYKDGKALKY-----WYENHNISITNATVEDSGTYCTG-----KWQLD 159
Qy 174 -PSDPLELV 182
Db 160 YESEPLNITV 169

RESULT 18
US-09-245-764-9
; Sequence 9, Application US/09245764
; Patent No. 6675105
; GENERAL INFORMATION:
; APPLICANT: Hogarth, P. Mark
; APPLICANT: Powell, Maree S.
```

APPLICANT: McKenzie, Ian F.C.  
APPLICANT: Maxwell, Kelly F.  
APPLICANT: Garrett, Thomas P.J.  
APPLICANT: Epa, Vidana  
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES AND MODELS OF FC RECEPTORS  
FILE REFERENCE: 4102-4  
CURRENT APPLICATION NUMBER: US/09/245,764  
CURRENT FILING DATE: 1999-02-05  
EARLIER APPLICATION NUMBER: 60/099,994  
EARLIER FILING DATE: 1998-09-11  
EARLIER APPLICATION NUMBER: 60/073,972  
EARLIER FILING DATE: 1998-02-06  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 9  
LENGTH: 172  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-245-764-9

Query Match 7.7%; Score 100; DB 4; Length 172;  
Best Local Similarity 24.7%; Pred. No. 0.049;  
Matches 47; Conservative 27; Mismatches 78; Indels 38; Gaps 9;

QY 6 PKPSLQALPSSLVPLEKPVTLRCQPGVDLYRLLEKLSRRY-----ODQAVLFIPA 57  
DB 5 PKVSLNP-PWNRIFKGENVTLTCG-----NNFEVSTTKWFHNGSLSEETNSLNI 57  
QY 58 MKRSLAGRYCYSYONGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLCQCTR 117  
DB 58 AKFEDSGEYKCHQO-----VNESEPVYLEVFSDWLLQLQASAEVVMGQPLFLRCHGW 110  
QY 118 YGFDQFAL--YKEDGPAPYKNPERWY-RASFPITVTAAHSGTYRCYCSFSSRDPVLSA- 173  
DB 111 RNWDVYKVIYKGEALKY-----WYENHNISITNAVEDSGTYCTG-----KVMQOLD 159  
QY 174 -PSDPLELV 182  
DB 160 YESEPLNITV 169

RESULT 19  
US-09-944-277A-13  
Sequence 13, Application US/09944277A  
Patent No. 6682894  
GENERAL INFORMATION:  
APPLICANT: Frank, Glenn R.  
Rushlow, Keith E.  
Wassom, Donald L.  
TITLE OF INVENTION: Method to Detect IgE  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Carol Talkington Verser, Ph.D.  
STREET: 1825 Sharp Point Drive  
CITY: Fort Collins  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80525  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: WordPerfect for Windows, Version 7.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/944,277A  
FILING DATE: 30-Aug-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/285,873  
FILING DATE: 1999-03-31

ATTORNEY/AGENT INFORMATION:  
NAME: Verser, Carol Talkington  
REGISTRATION NUMBER: 37,459  
REFERENCE/DOCKET NUMBER: DI-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 970/493-7272  
TELEFAX: 970/484-9505  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 172 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
US-09-944-277A-13

Query Match 7.7%; Score 100; DB 4; Length 172;  
Best Local Similarity 24.7%; Pred. No. 0.049;  
Matches 47; Conservative 27; Mismatches 78; Indels 38; Gaps 9;

QY 6 PKPSLQALPSSLVPLEKPVTLRCQPGVDLYRLLEKLSRRY-----ODQAVLFIPA 57  
DB 5 PKVSLNP-PWNRIFKGENVTLTCG-----NNFEVSTTKWFHNGSLSEETNSLNI 57  
QY 58 MKRSLAGRYCYSYONGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLCQCTR 117  
DB 58 AKFEDSGEYKCHQO-----VNESEPVYLEVFSDWLLQLQASAEVVMGQPLFLRCHGW 110  
QY 118 YGFDQFAL--YKEDGPAPYKNPERWY-RASFPITVTAAHSGTYRCYCSFSSRDPVLSA- 173  
DB 111 RNWDVYKVIYKGEALKY-----WYENHNISITNAVEDSGTYCTG-----KVMQOLD 159  
QY 174 -PSDPLELV 182  
DB 160 YESEPLNITV 169

RESULT 20  
US-08-756-387B-11  
Sequence 11, Application US/08756387B  
Patent No. 5945294  
GENERAL INFORMATION:  
APPLICANT: Frank, Glenn R.  
APPLICANT: Porter, James P.  
APPLICANT: Rushlow, Keith E.  
APPLICANT: Wassom, Donald L.  
TITLE OF INVENTION: Method to Detect IgE  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Carol Talkington Verser, Ph.D.  
ADDRESSEE: Heska Corporation  
STREET: 1825 Sharp Point Drive  
CITY: Fort Collins  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80525  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: WordPerfect for Windows, Version 7.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/756,387B  
FILING DATE: No. 5945294ember 26, 1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Verser, Carol Talkington  
REGISTRATION NUMBER: 37,459  
REFERENCE/DOCKET NUMBER: DI-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 970/493-7272  
TELEFAX: 970/484-9505  
INFORMATION FOR SEQ ID NO: 11:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 197 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-756-387B-11

Query Match          7.7%; Score 100; DB 2; Length 197;
Best Local Similarity 24.7%; Pred. No. 0.059;
Matches 47; Conservative 27; Mismatches 78; Indels 38; Gaps 9;

QY 6 PKPSLQALPSSLVLPLEKPVTLRCQGPVGLYRLKLSRSSRY-----QDQAVLFIPA 57
Db 30 PKVSLNP-PWNRIFKGENVTITCNG-----NNFEVSSSTKWFHNGSLSEETNSSLNIVN 82
QY 58 MKRSLAGRYCYSQNGSLWLSPLSDQLVLVATGVFAKPSLSAQPGPAVSSGGDVTLCQCTR 117
Db 83 AKFEDSGEYKCOHQ-----VNESEPVYLEVFSWLLQLQASAEVVMGQPLFLRCHGW 135
QY 118 YGFDQFAL--YKGDPAKYKNPERWY-RASFPITVTAAHSGTYRCYFSFSDRDPYLWSA- 173
Db 136 RNWDVYKVIYKGEALKY-----WYENHNISITNATVEDSGTYCYCTG-----KMWOLD 184
QY 174 -PSDPLELV 182
Db 185 YESEPLNITV 194

RESULT 21
US-09-285-873-11
; Sequence 11, Application US/09285873
; Patent No. 6309832
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect IgE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heeka Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/285,873
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387
; FILING DATE: No. 6309832ember 26, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 197 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-285-873-11
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 197 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-756-387B-11

Query Match          7.7%; Score 100; DB 3; Length 197;
Best Local Similarity 24.7%; Pred. No. 0.059;
Matches 47; Conservative 27; Mismatches 78; Indels 38; Gaps 9;

QY 6 PKPSLQALPSSLVLPLEKPVTLRCQGPVGLYRLKLSRSSRY-----QDQAVLFIPA 57
Db 30 PKVSLNP-PWNRIFKGENVTITCNG-----NNFEVSSSTKWFHNGSLSEETNSSLNIVN 82
QY 58 MKRSLAGRYCYSQNGSLWLSPLSDQLVLVATGVFAKPSLSAQPGPAVSSGGDVTLCQCTR 117
Db 83 AKFEDSGEYKCOHQ-----VNESEPVYLEVFSWLLQLQASAEVVMGQPLFLRCHGW 135
QY 118 YGFDQFAL--YKGDPAKYKNPERWY-RASFPITVTAAHSGTYRCYFSFSDRDPYLWSA- 173
Db 136 RNWDVYKVIYKGEALKY-----WYENHNISITNATVEDSGTYCYCTG-----KMWOLD 184
QY 174 -PSDPLELV 182
Db 185 YESEPLNITV 194

RESULT 22
US-09-944-277A-11
; Sequence 11, Application US/09944277A
; Patent No. 6682894
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect IgE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/944,277A
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 197 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-944-277A-11

Query Match          7.7%; Score 100; DB 4; Length 197;
Best Local Similarity 24.7%; Pred. No. 0.059;
Matches 47; Conservative 27; Mismatches 78; Indels 38; Gaps 9;
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Qy	6	PKPSLQALPSSLVLPLEKDVTLRCQPGPDVLYRLEKLSRRY-----QDOAVLFPA	57
Db	30	PKVSLNP-PWNRIPKGENVTLLTCNG-----NNFEVSTKWFHNGS:SEETNSSLNIWN	82
Qy	58	MKRSIAGRYRCSYQNGSLWSPSDQLELVATVCPAKPSLSAQPGPAVSGGDVTLQCQTR	117
Db	83	AKFDSGBYKQHQ-----VNESEPYLVEFSDWLLQASAEVWEGQPLF:RCHGW	135
Qy	118	YGFPQFAL--YKEGDPAPYKPNRWY-RASPIITVTAAHGTYRCYSFSSRDPYLWSA-	173
Db	136	RNWDVYKVIYKDGALXY----WYENHNISITNATVEDSGTYICTG-----KVMQLD	184
Qy	174	-PSDPLELVW	182
Db	185	YESEPLNITV	194

RESULT 23  
 US-07-869-933-13  
 ; Sequence 13, Application US/07869933  
 ; Patent No. 5770396  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KINET. Jean-Pierre  
 ; TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF  
 ; THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR  
 ; IMMUNOGLOBULIN  
 ; NUMBER OF SEQUENCES: 34  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Foley & Lardner  
 ; STREET: 1800 Diagonal Road, Suite 500  
 ; CITY: Alexandria  
 ; STATE: VA  
 ; COUNTRY: USA  
 ; ZIP: 22313-0299  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/869,933  
 ; FILING DATE: 19920416  
 ; CLASSIFICATION: 514  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: BENT, Stephen A.  
 ; REGISTRATION NUMBER: 29,768  
 ; REFERENCE/DOCKET NUMBER: 40399/154 NIHD  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (703)836-9300  
 ; TELEFAX: (703)683-4109  
 ; TELEX: 899149  
 ; INFORMATION FOR SEQ ID NO: 13:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 232 amino acids  
 ; TYPE: AMINO ACID  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: homo sapien  
 ; STRAIN: FCRI alpha subunit  
 ; US-07-869-933-13

	Query Match	7.7%;	Score 100;	DB 1;	Length 232;	
	Best Local Similarity	24.7%;	Pred. No. 0.075;			
	Matches	Conservative 27;	Mismatches 78;	Indels 38;	Gaps 9;	
QY	6	KPKSLQALPSSLVNPLEKPVTVTCQQPGVDLYRLEKLSRSSRY-----QDQAVLPIPA	57			
		: :     : :     : :     : :				
DG	5	PKVSLNP-PWNRIKFGENVTILTCNG-----NNPFVSSTKWFHFGSLSEETNSLNIVN	57			
QY	58	MKRSIAGRYRCSYQNGSLWSISPDQELVATGVAKPSLSAQPGPVAISSGGDVTLLOCOTR	117			
		: :     : :     : :     : :				
DG	58	AKFEDSGYKCOHQO-----VNSESPVYLVEFSDMILLQAASAEVVMEGQFLFRCHGW	110			
		: :     : :     : :     : :				

Qy 118 YGDFQAL--YKGDPAKYKPEWY-RASPLITVTTAAHSGTYRCYSFSSRDPYLWSA- 173  
Db 111 RNDVYKVIYKGEALKY-----WYENHNISITNAVEDSGTYCTG-----KWQLD 159

Qy 174 -PSDPLELV 182  
Db 160 YESEFLNIV 169

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1035
1036
1037
1038
1039
1040

```

Query Match	7.7%;	Score 100;	DB 2;	Length 232;
Best Local Similarity	24.7%;	Pred. No. 0.075;		
Matches	47;	Conservative	27;	Mismatches 78; Indels 38; Gaps 9;
Qy	6	PKPSLQALPSGLVPLEKPVTLRCQPGVDLRYLEKLSGRY-----QDOAVLRIPA	57	
Db	5	PKVSLNP-PWNRIPKGENVILTCNG-----NNFFEVSSITKWFHNGSLSEETNSSLNVN	57	
Qy	58	MKRSLAGRYRCSYNGSLWSPDQLDELVATGVPKFSLSAQOPGPNVSSGGDVTLOQOTR	117	
Db	58	AKFEDSGEYKCHQHQ-----VNESFVYLEVFSDWLLIQASAEVVMGQPLFLRCHGW	110	
Qy	118	YGFQDFAL--YKEGDPAFYKNPERWY--RAGSPIITVTAAHSGYRCYCSFSSRDPFLWSA-	173	
Db	111	RNWDYKVYYKGEALKY-----WYENHNISITNATVEDSGTYVCTG-----KMWQLD	159	
Qy	174	-PSDPLELVV	182	
Db	160	YESEFLNITY	169	

```

RESULT 25
US-09-103-663-13
; Sequence 13, Application US/09103663D
; Patent No. 6171803
; GENERAL INFORMATION:
; APPLICANT: Kinnet et al.
; TITLE OF INVENTION: Isolation, characterization, and use of the human beta
; TITLE OF INVENTION: subunit of the high affinity receptor for
; TITLE OF INVENTION: immunoglobulin E.
; FILE REFERENCE: 50490
; CURRENT APPLICATION NUMBER: US/09/103,663D
; CURRENT FILING DATE: 1998-06-23
; EARLIER APPLICATION NUMBER: 07/869,933
; EARLIER FILING DATE: 1992-04-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-09-103-663-13

Query Match      7.7%; Score 100; DB 3; Length 232;
Best Local Similarity 24.7%; Pred. No. 0.075;
Matches 47; Conservative 27; Mismatches 78; Indels 38; Gaps 9;

Qy 6 PKPSLQALPSSLVPLEKPVTLRCQGPFGVDLYRLKLSRRY-----QDQAVLFIPA 57
Db 5 PKVSLNP-PWNRIFKGENVTLCNG-----NNFFVSSTKWFHNGSLSEETNSSLNIVN 57
Qy 58 MKRSLAGRYRCYQNGSLWSLPDQLVLVATGVFAKPSLSAQPGPAVSSGGDVTLCQTR 117
Db 58 AKFEDSGEYKCHQO-----VNESEPVYLEVFSDWLLQLQASAEVVMGQPLFLRCHGW 110
Qy 118 YGPDQFAL--YKEGDPAPYKNPERWY-RASFPILITVTAHSGTYRCYSFSSRDPYLWSA- 173
Db 111 RNWDVYKVIYTKGEALKY-----WYENHNISITNATVEDSGTYTCG-----KMWQLD 159
Qy 174 -PSDPLELV 182
Db 160 YESEPLNITV 169

```

Search completed: October 29, 2005, 03:48:25  
Job time : 44 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 29, 2005, 03:33:47 ; Search time 167 Seconds  
(without alignments)  
576.667 Million cell updates/sec

Title: US-09-503-387-3\_COPY\_21\_269

Perfect score: 1304

Sequence: 1 QSGPLPFXSLQALPSSLVPL.....SPKESDSPAGPARQYTKGN 249

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 1541488

Minimum DB seq length: 0

Maximum DB seq length: 250

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A\_Geneseq\_16Dec04.\*

- 1: geneseqp1980s.\*
- 2: geneseqp1990s.\*
- 3: geneseqp2000s.\*
- 4: geneseqp2001s.\*
- 5: geneseqp2002s.\*
- 6: geneseqp2003as.\*
- 7: geneseqp2003bs.\*
- 8: geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1304	100.0	249	4	AAB61261 Human TAN
2	1304	100.0	249	6	ABU11227 Human TAN
3	970	74.4	203	5	AAO19266 Human pla
4	378.5	29.0	236	5	AAO19236 Human LIR
5	355.5	27.3	237	5	AAE19107 Human NKp
6	300	23.0	227	8	ADO24405 Human PRO
7	279.5	21.4	170	4	ABG10157 Novel hum
8	275.5	21.1	205	5	AAO19235 Human imm
9	272	20.9	74	4	AAO19235 Human pla
10	272	20.9	74	4	AAO19235 Human pla
11	268	20.6	47	4	AAO19235 Human TAN
12	268	20.6	47	6	ABU11227 Human TAN
13	245	18.8	228	5	AAO19267 Human Pcr
14	233	17.9	145	5	AAO19233 Human put
15	227.5	17.4	100	4	ABBA2669 Peptide #
16	227.5	17.4	100	4	AAO19233 Peptide #
17	227.5	17.4	100	4	AAO19233 Peptide #
18	227.5	17.4	100	4	AAO19233 Peptide #
19	227.5	17.4	100	4	AAO19233 Peptide #
20	227.5	17.4	100	4	AAO19233 Peptide #
21	227.5	17.4	100	5	ABG58080 Human bra
22	220	16.9	47	4	AAO19233 Peptide #
23	220	16.9	47	6	ABU11238 TANGO 268
24	218.5	16.8	221	8	ADK98546 Human imm
25	216.5	16.6	100	4	AAO19233 Peptide #

99	154	11.8	115	2	AAW78263	AAW78263 Fragment
100	154	11.8	120	2	AAW78154	AAW78154 Human sec
ALIGNMENTS						
RESULT 1						
AAB61261						
ID	AAB61261 standard; protein; 249 AA.					
XX	AC					
XX	AC	AAB61261;				
XX	DT	04-APR-2001 (first entry)				
XX	DE	Human TANGO 268 extracellular domain.				
XX	DE					
XX	KW	Human; TANGO 268; cardiant; cerebroprotective; cytostatic; anticoagulant;				
KW	KW	thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI;				
KW	KW	platelet membrane glycoprotein receptor; bleeding disorder;				
KW	KW	blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;				
KW	KW	ischaemia; cardiovascular disease; immunological disease; liver disorder;				
XX	KW	cancer.				
XX	OS	Homo sapiens.				
XX	FN	WO200100810-A1.				
XX	XX					
PD	PD	04-JAN-2001.				
XX	XX					
PF	PF	30-JUN-2000; 2000WO-US018152.				
XX	XX					
PR	PR	30-JUN-1999; 99US-00345468.				
XX	XX					
PR	PR	06-DEC-1999; 99US-00454824.				
XX	XX					
PR	PR	14-FEB-2000; 2000US-00503387.				
XX	XX					
PA	PA	(MILL-) MILLENNIUM PHARM INC.				
XX	XX					
PI	PI	Busfield SJ, Villelale J, Jandrot-Perrus M, Vainchencker W;				
PI	PI	Gill DS, Qian MD, Kingsbury G;				
XX	XX					
DR	DR	WPI; 2001-080877/09.				
XX	XX					
PT	PT	New genes encoding human platelet-expressed collagen receptor,				
PT	PT	glycoprotein VI, and its modulators, useful for preventing, treating and				
PT	PT	diagnosing hemorrhagic disorders, thrombotic diseases and immunological				
PT	PT	disorders.				
XX	XX					
PS	PS	Disclosure; Page 203-204; 227pp; English.				
XX	XX					
CC	CC	The present sequence is given in a specification relating to an isolated				
CC	CC	nucleic acid molecule encoding a platelet membrane glycoprotein receptor				
CC	CC	glycoprotein VI (GPVI), also called TANGO 268. The GPVI polynucleotides				
CC	CC	and polypeptides and their modulators, e.g. antisense nucleic acids,				
CC	CC	ribozymes and antibodies, are useful for preventing, treating and				
CC	CC	diagnosing disorders associated with aberrant expression or activity of				
CC	CC	GPVI. These disorders include bleeding disorders (e.g.				
CC	CC	thrombocytopaenia), blood vessel injury, thrombotic disorders (e.g.				
CC	CC	thrombotic occlusion of the coronary arteries), haemorrhagic disorders,				
CC	CC	coronary artery and cerebral artery diseases (e.g. stroke and ischaemia),				
CC	CC	cardiovascular diseases (e.g. atherosclerosis and myocardial infarction),				
CC	CC	immunological diseases (e.g. platelet disorder) and embryonic liver				
CC	CC	disorders. Preferably they are used to prevent acute cardiac ischaemia				
CC	CC	following angioplasty and metastatic cancers, especially of the colon and				
CC	CC	liver				
XX	XX					
SQ	SQ	Sequence 249 AA;				
Query Match						
Best Local Similarity		100.0%;		Score 1304; DB 4; Length 249;		
Matches 249; Conservative		100.0%;		Pred. No. 5.5e-105;		
		0; Mismatches		0; Indels		0; Gaps
						0;
QV	1	QSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPVDLYRLEKLSRSSRYQDQAVLFIPAMKR 60				

Db	1	QSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPVDLYRLEKLSRSSRYQDQAVLFIPAMKR	60
QY	61	SLAGRYRCSYQNGSLMSLPDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLCQTRYGF	120
Db	61	SLAGRYRCSYQNGSLMSLPDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLCQTRYGF	120
QY	121	DQFALYKEGDPAPYKPNRWYRASFPFIITVTAHSGTYRCYSFSSRDPYLWSAPSDPLEL	180
Db	121	DQFALYKEGDPAPYKPNRWYRASFPFIITVTAHSGTYRCYSFSSRDPYLWSAPSDPLEL	180
QY	181	VVTGTSVTPSRLPTEPPSSVAEFSEATAELTVSFNTKVFVTTTSRSTTSPKESDSPAGP	240
Db	181	VVTGTSVTPSRLPTEPPSSVAEFSEATAELTVSFNTKVFVTTTSRSTTSPKESDSPAGP	240
QY	241	ARQYTTKGN 249	
Db	241	ARQYTTKGN 249	
RESULT 2			
ABU11227			
ID	ABU11227 standard; peptide; 249 AA.		
XX	ABU11227;		
XX			
DT	06-FEB-2003 (first entry)		
XX			
DE	Human TANGO 268 extracellular domain.		
XX			
KW	Human; mouse; variable heavy; VH; antigen; cancer;		
KW	complementarity determining region; TANGO 268; glycoprotein VI; GPVI;		
KW	TANGO 268; extracellular matrix; collagen; platelet release;		
KW	proliferation; migration; embryogenesis; inflammation; thrombosis;		
KW	degranulation; thrombocytopaenia; antibody; thrombotic disorder;		
KW	cerebral vascular disease; stroke; ischaemia; venous thromboembolism;		
KW	leg swelling; pain; ulceration; pulmonary embolism; coronary disease;		
KW	cardiovascular disease; angina pectoris; myocardial infarction;		
KW	coronary restenosis; atherosclerosis; immunological disorder;		
KW	developmental disorder; embryonic disorder; liver disorder;		
KW	cerebral vascular disease; venous thromboembolism disease.		
OS	Homo sapiens.		
XX			
FN	WO200280968-A1.		
XX			
PD	17-OCT-2002.		
XX			
PF	09-APR-2002; 2002WO-US011122.		
XX			
PR	09-APR-2001; 2001US-00829495.		
XX			
PA	(MILL-) MILLENNIUM PHARM INC.		
XX			
PI	Busfield SJ, Villeval J, Jandrot-Perrus M, Vainchencker W;		
PI	Gill DS, Qian DM, Kingsbury G;		
XX			
DR	WPI; 2003-058477/05.		
XX			
PT	Novel substantially purified antibody immunospecifically binding to TANGO		
PT	268 antigen, useful for treating bleeding disorders such as		
PT	thrombocytopenia, stroke, ischemia, pulmonary embolism, atherosclerosis.		
XX			
PS	Disclosure; Page 212-213; 236pp; English.		
XX			
CC	This invention relates to a novel purified antibody comprising a variable		
CC	heavy (VH) complementarity determining region (CDR)1, VH CDR2 or VH CDR3;		
CC	or variable light (VL) CDR1, VL CDR2 or VL CDR3, and immunospecifically		
CC	binding to a TANGO 268 (also referred as glycoprotein VI (GpVI)) antigen.		
CC	The antibodies of the invention act to decrease or block TANGO 268		
CC	binding to extracellular matrix components, or as a Collagen or platelet		
CC	release and aggregation blocker. The antibodies of the invention are		
CC	useful for modulating proliferation, migration, morphology		

CC differentiation and/or function of megakaryocytes and platelets.  
 CC including during development e.g. embryogenesis, modulating leukocyte-  
 CC platelet and platelet-endothelium interactions in inflammation and/or  
 CC thrombosis, and modulating platelet aggregation and degradation. They  
 CC are also useful for modulating disorders associated with abnormal or  
 CC aberrant megakaryocyte and/or platelet proliferation, migration,  
 CC morphology, differentiation and/or function, e.g. bleeding disorders such  
 CC as thrombocytopenia. Other diseases which may be modulated by these  
 CC antibodies are thrombotic disorders, cerebral vascular diseases (e.g.  
 CC stroke and ischaemia) venous thromboembolism diseases (e.g. diseases  
 CC involving leg swelling, pain and ulceration, pulmonary embolism, etc);  
 CC coronary diseases (e.g. cardiovascular diseases including angina  
 CC pectoris, myocardial infarction, coronary restenosis, atherosclerosis,  
 CC etc); immunological disorders, developmental disorders, embryonic  
 CC disorders, liver diseases, cerebral vascular diseases, venous  
 CC thromboembolism diseases, coronary diseases, and metastatic cancers. The  
 CC antibodies of the invention only causes a transient decrease in platelet  
 CC counts, platelet aggregation, and/or platelet activation and so have some  
 CC advantages over prior art methods. The present sequence represents a  
 CC peptide sequence used to generate the antibodies of the invention  
 XX  
 SQ Sequence 249 AA;

Query Match 100.0%; Score 1304; DB 6; Length 249;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-105; Mismatches 0; Indels 0; Gaps 0;  
 Matches 249; Conservative 0;

QY 1 QSGPLPKPSLQALPSSLVPLKPVTLRCQGGVLDYLRLEKLSRSSRYQDQAVLFIPAMKR 60  
 DB 1 QSGPLPKPSLQALPSSLVPLKPVTLRCQGGVLDYLRLEKLSRSSRYQDQAVLFIPAMKR 60  
 QY 61 SLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGVAVSSGGDVTLCQTRYGF 120  
 DB 61 SLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGVAVSSGGDVTLCQTRYGF 120  
 QY 121 DQFALYKEGDPAPYKPNRWYRASPIITVTAHSGTYRCYFSFSSRDYPLWSAPSDPLEL 180  
 DB 121 DQFALYKEGDPAPYKPNRWYRASPIITVTAHSGTYRCYFSFSSRDYPLWSAPSDPLEL 180  
 QY 181 VVTGTSVTPSRLLTPPPSSVAEFSBATAELTVSFNKTFTTTSRITTSPPKESDSPAGP 240  
 DB 181 VVTGTSVTPSRLLTPPPSSVAEFSBATAELTVSFNKTFTTTSRITTSPPKESDSPAGP 240  
 QY 241 ARQYVTKGN 249  
 DB 241 ARQYVTKGN 249

RESULT 3  
 AAO19266  
 ID AAO19266 standard; protein; 203 AA.

XX AAO19266;  
 XX  
 XX 27-NOV-2002 (first entry)  
 XX  
 XX Human platelet glycoprotein VI-2 protein SEQ ID NO: 75.  
 XX  
 XX Human; leukocyte immunoglobulin receptor-like protein; LIR-like protein;  
 KW vulnary; neuroprotective; anti-inflammatory; cerebroprotective;  
 KW nutritional supplement; lymphoid disorder; burn; wound; ulcer; stroke;  
 KW Alzheimer's disease; amyotrophic lateral sclerosis; fibrosis; cancer;  
 KW immune disorder; multiple sclerosis; allergy; inflammation; infertility;  
 KW cytostatic; immunosuppressive; anti-diabetic; antiinfertility.  
 XX  
 XX Homo sapiens.  
 XX  
 XX WO200266600-A2.  
 XX  
 XX 29-AUG-2002.  
 XX  
 XX 28-DEC-2001; 2001WO-US049435.

PR 29-DEC-2000; 2000US-00751518.  
 XX (HYSE-) HYSEQ INC.  
 XX  
 XX Boyle BJ, Kuo C, Mize NK, Haley-Vicente DA, Arterburn MC;  
 XX Tang YT, Zhou P, Liu C, Asundi V, Drmanac RT, Yeung G, Palencia S;  
 XX WPI; 2002-674924/72.  
 XX  
 XX New leukocyte immunoglobulin receptor-like (LIR-like) polynucleotides and  
 XX polypeptides, useful in research, as nutritional sources, or for treating  
 XX wounds, Alzheimer's disease, inflammations, infertility, stroke or  
 XX cancers.

XX Example 5; Page 213; 215pp; English.

XX The present invention provides the protein and coding sequences of human  
 XX leukocyte immunoglobulin receptor-like molecules. These can be used as  
 XX nutritional sources or supplements, or for treating myeloid or lymphoid  
 XX disorders, burns, wounds, ulcers, Alzheimer's disease, amyotrophic  
 XX lateral sclerosis, lung or liver fibrosis, immune disorders such as  
 XX severe combined immunodeficiency, multiple sclerosis, allergies, graft-  
 XX versus-host disease, inflammations, infertility, stroke, or cancers. The  
 XX present sequence is a polypeptide described in the exemplification of the  
 XX invention

XX Sequence 203 AA;

Query Match 74.4%; Score 970; DB 5; Length 203;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-76;  
 Matches 183; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSGPLPKPSLQALPSSLVPLKPVTLRCQGGVLDYLRLEKLSRSSRYQDQAVLFIPAMKR 60  
 DB 21 QSGPLPKPSLQALPSSLVPLKPVTLRCQGGVLDYLRLEKLSRSSRYQDQAVLFIPAMKR 80  
 QY 61 SLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGVAVSSGGDVTLCQTRYGF 120  
 DB 81 SLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGVAVSSGGDVTLCQTRYGF 140  
 QY 121 DQFALYKEGDPAPYKPNRWYRASPIITVTAHSGTYRCYFSFSSRDYPLWSAPSDPLEL 180  
 DB 141 DQFALYKEGDPAPYKPNRWYRASPIITVTAHSGTYRCYFSFSSRDYPLWSAPSDPLEL 200  
 QY 181 VVT 183  
 DB 201 VVT 203

RESULT 4  
 AAO19236  
 ID AAO19236 standard; protein; 236 AA.

XX AAO19236;  
 XX  
 XX 27-NOV-2002 (first entry)  
 XX  
 XX Human LIR-pbm36-2 protein SEQ ID NO: 32.  
 XX  
 XX Human; leukocyte immunoglobulin receptor-like protein; LIR-like protein;  
 KW vulnary; neuroprotective; anti-inflammatory; cerebroprotective;  
 KW nutritional supplement; lymphoid disorder; burn; wound; ulcer; stroke;  
 KW Alzheimer's disease; amyotrophic lateral sclerosis; fibrosis; cancer;  
 KW immune disorder; multiple sclerosis; allergy; inflammation; infertility;  
 KW cytostatic; immunosuppressive; anti-diabetic; antiinfertility.  
 XX  
 XX Homo sapiens.  
 XX  
 XX WO200266600-A2.  
 XX  
 XX 29-AUG-2002.  
 XX  
 XX 28-DEC-2001; 2001WO-US049435.

```

XX 29-DEC-2000; 2000US-00751518.
XX (HYSE-) HYSEQ INC.
XX Boyle BJ, Kuo C, Mize NK, Haley-Vicente DA, Arterburn MC;
XX Tang YT, Zhou P, Liu C, Asundi V, Drmanac RT, Yeung G, Palencia S;
XX WPI; 2002-674924/72.
XX New leukocyte immunoglobulin receptor-like (LIR-like) polynucleotides and
XX polypeptides, useful in research, as nutritional sources, or for treating
XX wounds, Alzheimer's disease, inflammations, infertility, stroke or
XX cancers.
XX Example 5; Page 190-191; 215pp; English.
XX The present invention provides the protein and coding sequences of human
XX leukocyte immunoglobulin receptor-like molecules. These can be used as
XX nutritional sources or supplements, or for treating myeloid or lymphoid
XX disorders, burns, wounds, ulcers, Alzheimer's disease, amyotrophic
XX lateral sclerosis, lung or liver fibrosis, immune disorders such as
XX severe combined immunodeficiency, multiple sclerosis, allergies, graft-
XX versus-host disease, inflammations, infertility, stroke, or cancers. The
XX present sequence is a polypeptide described in the exemplification of the
XX invention
XX Sequence 236 AA;
XX
XX Query Match 29.0%; Score 378.5; DB 5; Length 236;
XX Best Local Similarity 41.7%; Pred. No. 1.5e-24;
XX Matches 91; Conservative 33; Mismatches 73; Indels 21; Gaps 7;
XX
XX Qy 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPPGVDLYRL--EKLSS---SRYQDAV--- 52
XX Db 22 QAGTLRPKPTLWAEFGSVITQSSPVTLMCGQILETQEVRLYREKKTAPWITRPOEIVKKG 81
XX
XX Qy 53 -LFTPAKMSLAGRYRCSYQNGSL-WSLPDQLBELVATGVFAKPSLSAQPGPAVSSGDV 110
XX Db 82 QFPIPSITWEHTGRYRCFYGSHTAGWSEPSDPLELVVTGAYIKFTLSALPSPVVTSGNV 141
XX
XX Qy 111 TLQCTQRYGDFQFALYKEGD---PAPYKNPGR---WVRASPIITVTAAHSGTYRCYSFS 164
XX Db 142 TLHCVSQVAFGSFLCKEGEDEHFCQLNSQPRTHGWSRAIPSGVPSFRWSRYRCYAYD 201
XX
XX Qy 165 SRDPLMSAPSDPLELVVTGTSVTPSRLPTEPPSSVAE 202
XX Db 202 SNSPHVMSLPDLELLVPGAAETLS-----PPQNKSD 234
XX
XX RESULT 5
XX AAEE19107
XX ID AAEE19107 standard; protein; 237 AA.
XX AC AAEE19107;
XX XX
XX DT 21-MAY-2002 (first entry)
XX XX
XX DE Human NKp46 (isoform b) protein.
XX XX
XX KW Human; natural killer cell activating protein; NKp46; therapy; virucide;
XX KW viral infection; natural killer cell; NK; NKp44; imaging agent; cancer;
XX KW detection; carcinoma; melanoma; lymphoma; sarcoma; cytostatic.
XX XX
XX OS Homo sapiens.
XX XX
XX PN WO200208287-A2.
XX XX
XX PD 31-JAN-2002.
XX XX
XX PF 19-JUL-2001; 2001WO-IL000664.
XX XX
XX PR 20-JUL-2000; 2000IL-00137419.

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XX (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
XX (UYNE ) UNIV BEN-GURION NEGEV.
XX Mandelboim O, Porgador A;
XX WPI; 2002-195870/25.
XX N-PSDB; AAD30464.
XX
XX New targeting complex capable of targeting an active substance to a
XX target cell, comprising a target recognition segment and an active
XX segment, useful for treating pathologies associated with viral infections
XX or cancer.
XX Claim 3; Page 104-105; 113pp; English.
XX
XX The invention relates to compositions and methods for the treatment and
XX detection of a variety of viral infections, by using complex agents
XX comprising the natural killer (NK) cells activating proteins, NKp46 and
XX NKp44 and functional fragments thereof, linked to therapeutic or imaging
XX agents. The complex is useful for treating pathologies associated with
XX viral infections (e.g. infections caused by influenza virus, HIV, Epstein
XX -Barr virus, cytomegalovirus, vaccinia virus, ECMV, MVM or herpes virus)
XX and cancer (e.g. carcinomas, melanomas, lymphomas and sarcomas), and for
XX the imaging and monitoring of cancer. The complex may also be used to
XX detect the presence of abnormal cells in a sample. The antibodies can be
XX used to qualitatively or quantitatively detect the ligand for the
XX complex. The present sequence is human NKp46 (isoform b) protein
XX
XX Sequence 237 AA;
XX
XX Query Match 27.3%; Score 355.5; DB 5; Length 237;
XX Best Local Similarity 38.4%; Pred. No. 1.5e-22;
XX Matches 81; Conservative 30; Mismatches 77; Indels 23; Gaps 3;
XX
XX Qy 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPPGVDLYRL-----EKLSSS 45
XX Db 22 QOQTLKPFTWAEFHWPFKQVTCQNGYAGVEYQLHFEGLFAVDPRPKPERINKV 81
XX
XX Qy 46 RYDQDAVLFTPAKMSLAGRYRCSYQNGSLWSPDQLBELVATGVFAKPSLSAQPGPAVS 105
XX Db 82 KF-----YIPDMNSRMAGQYSCIYRVGELWSEPSNLLDLVVTMDYDTPLSVHPGPEVI 135
XX
XX Qy 106 SGGDVTLCQCTRYGDFQFALYKEGDPAFYKNPWRWYRASPIITVTAAHSGTYRCYSFS 165
XX Db 136 SGEKVTPTYCRDLDTATSNMFLLLKGRSHVQGVKGVAEPFLGPVTTAHRGTYRC--FGS 193
XX
XX Qy 166 RDPYLSAPSDPLELVVTGTSVTPSRLPTEP 196
XX Db 194 YNNHWSFPSEPVKLLVTGDIENSLAPEDP 224
XX
XX RESULT 6
XX ADO24405
XX ID ADO24405 standard; protein; 227 AA.
XX AC ADO24405;
XX XX
XX DT 12-AUG-2004 (first entry)
XX XX
XX DE Human PRO87333 protein SEQ ID NO:44.
XX XX
XX KW human; PRO; antianaemic; antiarthritic; antiinflammatory; antipsoriatic;
XX KW antirheumatic; dermatological; immunostimulant; immunosuppressive;
XX KW osteopathic; vasotropic; immune related disease;
XX KW inflammatory immune response; rheumatoid arthritis;
XX KW juvenile chronic arthritis; systemic lupus erythematosus;
XX KW spondyloarthropathy; systemic sclerosis;
XX KW idiopathic inflammatory myopathy; Sjogren's syndrome;
XX KW systemic vasculitis; sarcoidosis; autoimmune haemolytic anaemia;
XX KW autoimmune disease; immune-mediated skin disease; bullous skin disease;
XX KW erythema multiforme; contact dermatitis; psoriasis; lymphadenopathy;
XX KW splenomegaly; leukopaenia.

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XX OS Homo sapiens.  
XX PN WO2004043397-A2.  
XX PD 27-MAY-2004.  
XX PF 12-NOV-2003; 2003WO-US036002.  
XX PR 12-NOV-2002; 2002US-0425931P.  
XX PA (GETH ) GENENTECH INC.  
XX PI Abbas A, Bodary S, Clark H, Wu TD, Schoenfeld J, Wood WI;  
XX DR WPI; 2004-420080/39.  
XX DR N-PSDB; ADO24404.  
XX New isolated PRO polypeptide e.g. PRO37544, PRO69493, PRO87327 etc,  
XX capable of stimulating an immune response, useful for treating diseases  
XX such as rheumatoid arthritis, psoriasis, and leukopenia.  
XX  
XX Claim 9; SEQ ID NO 44; 326pp; English.  
XX  
XX The present invention describes an isolated human PRO polypeptide (I).  
XX Also described: (1) an isolated PRO nucleic (II) acid encoding (I); (2) a  
XX vector (III) comprising (II); (3) a host cell (IV) comprising (III); (4)  
XX producing (I); (5) a chimeric molecule (V) comprising (I) fused to a  
XX heterologous amino acid sequence; (6) an antibody (VI) which specifically  
XX binds to (I); (7) a composition of matter comprising (I), an agonist of  
XX (I), an antagonist of (I), or (VI) in combination with a carrier; (8)  
XX treating (M1) an immune related disorder in a mammal, by administering  
XX (I), an agonist of (I), an antagonist of (I), or the antibody (VI); (9)  
XX diagnosing an immune related disease in a mammal, by detecting the level  
XX of expression of a gene encoding (I) in a test sample of tissue cells  
XX obtained from the mammal and in a control sample of known normal tissue  
XX cells of the same cell type; (10) identifying a compound that inhibits the  
XX activity of (I); (11) identifying a compound (M2) that inhibits the  
XX expression of a gene encoding (I); (12) identifying a compound that  
XX mimics the activity of (I); and (12) stimulating the immune response in a  
XX mammal, by administering (I) or its antagonist to the mammal. (I) has  
XX antianemic, antiarthritic, antiinflammatory, antipsoriatic,  
XX antirheumatic, dermatological, immunostimulant, immunosuppressive,  
XX osteoprotic and vasotropic activities. (I) and (VI) are useful for  
XX diagnosing an immune related disease in a mammal. (II) is useful for  
XX diagnosing an inflammatory immune response in a mammal. (VI) is useful  
XX for determining the presence of (I) in a sample suspected of containing  
XX the polypeptide. (M1) is useful for treating mammal having an immune  
XX related disorder chosen from rheumatoid arthritis, osteoarthritis,  
XX juvenile chronic arthritis, systemic lupus erythematosus  
XX spondyloarthropathies, systemic sclerosis, idiopathic inflammatory  
XX myopathies, Sjogren's syndrome, systemic vasculitis, sarcoidosis,  
XX autoimmune haemolytic anaemia, autoimmune or immune-mediated skin  
XX diseases including bullous skin diseases, erythema multiforme and contact  
XX dermatitis, psoriasis, lymphadenopathy, splenomegaly and leukopenia. The  
XX present sequence represents a human PRO protein from the present  
XX invention.  
XX  
XX Sequence 227 AA;  
XX  
Query Match 23.0%; Score 300; DB 8; Length 227;  
Best Local Similarity 36.6%; Pred. No. 9.4e-18;  
Matches 71; Conservative 34; Mismatches 77; Indels 12; Gaps 2;  
QY 3 GPLPKFSLQALPSSLVPLEKPTLRQCGPPGVLDLYRLEKLSRRYQD-----QA 51  
DB 12 GDFPFPFIAKSSPVLPDGSVKIQCAIREAVLTQLMIKNTYREIGRLKFWNETDP 71  
QY 52 VLFIPAKKSLAGRYRCSTQNSLWLSLPDQLELVATGVFAKPSLSAQPGPAVSSGDDVT 111  
DB 72 EFVIDHMDANKAGRYCQVRIHYRFRYSDTLELVVTGLYKGFSLADRLGLVMPGENTIS 131  
QY 112 LQCFTRY-GFDQFALYKEGDPAPYKPNRWYRSPFIITVTAHSGTYRCYSFSSRDPLY 170

Db 132 LTCSSAHIPDFRFLAKEGELSLPQHSGEHPANFSLGPDVNLVNSYRCYGTWNRSPYL 191  
QY 171 WSAFSDPLELVVTG 184  
DB 192 WSPFSALELVVTG 205  
RESULT 7  
ABGI0157  
ID ABGI0157 standard; protein; 170 AA.  
XX AC ABGI0157;  
XX DT 13-FEB-2002 (first entry)  
XX DE Novel human diagnostic protein #10148.  
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;  
XX KW food supplement; medical imaging; diagnostic; genetic disorder.  
XX OS Homo sapiens.  
XX PN WO200175067-A2.  
XX PD 11-OCT-2001.  
XX PF 30-MAR-2001; 2001WO-US008631.  
XX PR 31-MAR-2000; 2000US-00540217.  
XX PR 23-AUG-2000; 2000US-00649167.  
XX (HYSE-) HYSEQ INC.  
XX PA Drmanac RT, Liu C, Tang YT;  
XX PI WPI; 2001-639362/73.  
XX DR N-PSDB; AAS74344.  
XX New isolated polynucleotide and encoded polypeptides, useful in  
XX diagnostics, forensics, gene mapping, identification of mutations  
XX responsible for genetic disorders or other traits and to assess  
XX biodiversity.  
XX Claim 20; SEQ ID NO 40516; 103pp; English.  
XX  
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)  
XX sequences. (I) is useful as hybridisation probes, polymerase chain  
XX reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
XX and in recombinant production of (II). The polynucleotides are also used  
XX in diagnostics as expressed sequence tags for identifying expressed  
XX genes. (I) is useful in gene therapy techniques to restore normal  
XX activity of (II) or to treat disease states involving (II). (II) is  
XX useful for generating antibodies against it, detecting or quantitating a  
XX polypeptide in tissue, as molecular weight markers and as a food  
XX supplement. (II) and its binding partners are useful in medical imaging  
XX of sites expressing (II). (I) and (II) are useful for treating disorders  
XX involving aberrant protein expression or biological activity. The  
XX polypeptide and polynucleotide sequences have applications in  
XX diagnostics, forensics, gene mapping, identification of mutations  
XX responsible for genetic disorders or other traits to assess biodiversity  
XX and to produce other types of data and products dependent on DNA and  
XX amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic  
XX amino acid sequences of the invention. Note: The sequence data for this  
XX patent did not appear in the printed specification, but was obtained in  
XX electronic format directly from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 170 AA;  
XX  
Query Match 21.4%; Score 279.5; DB 4; Length 170;  
Best Local Similarity 37.7%; Pred. No. 3.9e-16;  
Matches 72; Conservative 22; Mismatches 56; Indels 41; Gaps 7;

Qy 7 KPSLQALPSSLVPLEKPVTLRCQPPGVDLVRLKLSRSSRYQDAVLFIPIAMKRSLAGRY 66  
Db 7 KPSFLALPGHLVKEETVILQCSVDNMFHFLLHR-----EGTY 45  
Qy 67 RC-----SVQNGSLWSLPSDQLELVATGVFAKPSLSAOPGPAVSSGGDVTLQCOIRYG 119  
Db 46 RCYGSVPHPYQ-----USAPSDPLDMVILIGYKPSLSAOPGPTVQAGENVTLSCSRSS 101  
Qy 120 FQOPALYKEGDPAPYKNP-----ERWRASFPPIITVTAHSGTYRCYCSFSSRD--PYLWSA 173  
Db 102 YDMVHLSREGEAHERRLPAVRSGINGTQADPPL--GPATGGTYRCFG-SFRDAPYEWNS 158  
Qy 174 PSDPLELVVTG 184  
Db 159 SSDPLLVSVTG 169

RESULT 8  
AAO19235  
ID AAO19235 standard; protein; 205 AA.  
XX  
AC AAO19235;  
XX  
DT 27-NOV-2002 (first entry)  
XX  
DE Human immunoglobulin-like protein IGSF1 SEQ ID NO: 31.  
XX  
KW Human; leukocyte immunoglobulin receptor-like protein; LIR-like protein;  
KW vulnery; neuroprotective; anti-inflammatory; cerebroprotective;  
KW nutritional supplement; lymphoid disorder; burn; wound; ulcer; stroke;  
KW Alzheimer's disease; ankyrotrophic lateral sclerosis; fibrosis; cancer;  
KW immune disorder; multiple sclerosis; allergy; inflammation; infertility;  
KW cytosatic; immunosuppressive; anti-diabetic; antiinfertility.  
XX  
OS Homo sapiens.  
XX  
FN WO200266600-A2.  
XX  
PD 29-AUG-2002.  
XX  
PF 28-DEC-2001; 2001WO-US049435.  
XX  
PR 29-DEC-2000; 2000US-00751518.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Boyle BJ, Kuo C, Mize NK, Haley-Vicente DA, Arterburn MC;  
PI Tang YT, Zhou P, Liu C, Asundi V, Drmanac RT, Yeung G, Palencia S;  
XX  
DR WPI; 2002-674924/72.  
XX  
PT New leukocyte immunoglobulin receptor-like (LIR-like) polynucleotides and  
PT polypeptides, useful in research, as nutritional sources, or for treating  
PT wounds, Alzheimer's disease, inflammations, infertility, stroke or  
XX cancers.  
XX  
PS Example 5; Page 189-190; 215pp; English.  
XX  
CC The present invention provides the protein and coding sequences of human  
CC leukocyte immunoglobulin receptor-like molecules. These can be used as  
CC nutritional sources or supplements, or for treating myeloid or lymphoid  
CC disorders, burns, wounds, ulcers, Alzheimer's disease, ankyrotrophic  
CC lateral sclerosis, lung or liver fibrosis, immune disorders such as  
CC severe combined immunodeficiency, multiple sclerosis, allergies, graft-  
CC versus-host disease, inflammations, infertility, stroke, or cancers. The  
CC present sequence is a polypeptide described in the exemplification of the  
XX invention

Qy 7 KPSLQALPSSLVPLEKPVTLRCQGP---PGVDLYRLKLSRSSRY-----ODQAVLFIPIAM 58  
Db 1 PKPWLFAEPSSVVPVPMGQNTVLCRGPVHGVGYILHKEGEATSMQLMGSTNDGAPFITNI 60  
Qy 59 KRSILAGRYCSYQ--NGSLWSLPSDQLELVATGVFAKPSLSAOPGPAVSSGGDVTLQCC 115  
Db 61 SGYSMGRIYSCYHPDWTSSIKIOPSNTLELVTLGLLPKPSLLAOPGPAVSGENVTLQCC 120  
Qy 116 TRYGFDFQALYKEG--DPAPYKNPFRWYRASFPPIITVTAHSGTYRCYCSFSSRDPYLWSA 173  
Db 121 GELPDSTFVLLKEGAQEPLEQQRPS--GYRADFWMPAVRGEDSGIYSCVYLDSTPFAASN 179  
Qy 174 PSDPLELVVTGTSVTPS 190  
Db 180 HSDSLEIWTVDKPKPS 196

RESULT 9  
AAAY72789  
ID AAY72789 standard; protein; 74 AA.  
XX  
AC AAY72789;  
XX  
DT 31-MAY-2001 (first entry)  
XX  
DE Human platelet membrane glycoprotein VI (GPVI) partial protein #b.  
XX  
KW Human; platelet membrane glycoprotein VI; GPVI; thrombolytic; therapy;  
KW vascular disease; thrombosis.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 15 /note= "Encoded by CYG"  
FT  
XX  
FN WO200116321-A1.  
XX  
PD 08-MAR-2001.  
XX  
PF 01-SEP-2000; 2000WO-US023975.  
XX  
PR 01-SEP-1999; 99US-0152197P.  
PR 08-OCT-1999; 99US-0158251P.  
XX  
PA (SAKA ) OTSUKA PHARM CO LTD.  
XX  
PI Tandon N, Sun B, Nakamura T, Yamamoto N;  
XX  
DR WPI; 2001-226691/23.  
DR N-PSDB; AAD02854.  
XX  
PT Anti-thrombotic medicament, comprising a polypeptide having the  
PT extracellular domain of platelet membrane glycoprotein VI or its variant,  
PT useful for treating a vascular disease and reducing platelet activation.  
XX  
PS Disclosure; Fig 2; 74pp; English.  
XX  
CC The present sequence is a human platelet membrane glycoprotein VI (GPVI)  
CC partial protein #b. The medicament comprising GPVI is useful for treating  
CC vascular disease, and for reducing platelet activation which involves  
CC contacting platelets with the medicament. The extracellular portion of  
CC GPVI is used therapeutically to attenuate platelet activation and  
CC aggregation and to treat thrombosis and other vascular diseases.  
CC Antibodies generated against GPVI are used as research and  
XX immunotherapeutic agents

Qy Sequence 74 AA;  
XX

Query Match 20.9%; Score 272; DB 4; Length 74;  
Best Local Similarity 98.1%; Pred. No. 5.9e-16;

```
Matches 53; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQPGVDLYRLEKLSRSSRYDQAVLF 54
Db 21 QSGPLPKPSLQALPSSLVPLEKPVTLRCQPGVDLYRLEKLSRSSRYDQAVLF 74
RESULT 10
AAY72788
ID AAY72788 standard; protein; 74 AA.
XX
AC AAY72788;
XX
XX 31-MAY-2001 (first entry)
XX
DE Human platelet membrane glycoprotein VI (GPVI) partial protein #a.
XX
KW Human; platelet membrane glycoprotein VI; GPVI; thrombolytic; therapy;
KW vascular disease; thrombosis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 15
FT /note= "Encoded by CYG"
XX
XX WO200116321-A1.
XX
XX 08-MAR-2001.
XX
XX 01-SEP-2000; 2000WO-US023975.
XX
XX 01-SEP-1999; 99US-0152197P.
XX 08-OCT-1999; 99US-0158251P.
XX
XX (SAKA ) OTSUKA PHARM CO LTD.
XX
XX Tandon N, Sun B, Nakamura T, Yamamoto N;
XX
XX WPI; 2001-226691/23.
XX N-PSDB; AAD02854.
XX
XX Anti-thrombotic medicament, comprising a polypeptide having the
XX extracellular domain of platelet membrane glycoprotein VI or its variant,
XX useful for treating a vascular disease and reducing platelet activation.
XX
XX Claim 11; Fig 2; 74pp; English.
XX
XX The present sequence is a human platelet membrane glycoprotein VI (GPVI)
XX partial protein #a. The medicament comprising GPVI is useful for treating
XX vascular disease, and for reducing platelet activation which involves
XX contacting platelets with the medicament. The extracellular portion of
XX GPVI is used therapeutically to attenuate platelet activation and
XX aggregation and to treat thrombosis and other vascular diseases.
XX Antibodies generated against GPVI are used as research and
XX immunotherapeutic agents
XX
XX Sequence 74 AA;
Query Match 20.9%; Score 272; DB 4; Length 74;
Best Local Similarity 98.1%; Pred. No. 5.9e-16;
Matches 53; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQPGVDLYRLEKLSRSSRYDQAVLF 54
Db 21 QSGPLPKPSLQALPSSLVPLEKPVTLRCQPGVDLYRLEKLSRSSRYDQAVLF 74
RESULT 11
AAB61259
ID AAB61259 standard; protein; 47 AA.
XX
XX AAB61259;
```

```
XX
DT 04-APR-2001 (first entry)
XX
XX Human TANGO 268 Ig-like domain #2.
XX
XX Human; TANGO 268; cardiant; cerebroprotective; cytostatic; anticoagulant;
XX thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI;
XX platelet membrane glycoprotein receptor; bleeding disorder;
XX blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;
XX ischaemia; cardiovascular disease; immunological disease; liver disorder;
XX cancer.
XX
XX Homo sapiens.
XX
XX WO200100810-A1.
XX
XX 04-JAN-2001.
XX
XX 30-JUN-2000; 2000WO-US018152.
XX
XX 30-JUN-1999; 99US-00345468.
XX 06-DEC-1999; 99US-00454824.
XX 14-FEB-2000; 2000US-00503387.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Busfield SJ, Vilelial J, Jandrot-Perrus M, Vainchencker W;
XX Gill DS, Qian WD, Kingsbury G;
XX
XX WPI; 2001-080877/09.
XX
XX New genes encoding human platelet-expressed collagen receptor,
XX glycoprotein VI, and its modulators, useful for preventing, treating and
XX diagnosing hemorrhagic disorders, thrombotic diseases and immunological
XX disorders.
XX
XX Disclosure; Page 203; 227pp; English.
XX
XX The present sequence is given in a specification relating to an isolated
XX nucleic acid molecule encoding a platelet membrane glycoprotein receptor
XX glycoprotein VI (GPVI), also called TANGO 268. The GPVI polynucleotides
XX and polypeptides and their modulators, e.g. antisense nucleic acids,
XX ribozymes and antibodies, are useful for preventing, treating and
XX diagnosing disorders associated with aberrant expression or activity of
XX GPVI. These disorders include bleeding disorders (e.g.
XX thrombocytopenia), blood vessel injury, thrombotic disorders (e.g.
XX thrombotic occlusion of the coronary arteries), haemorrhagic disorders,
XX coronary artery and cerebral artery diseases (e.g. stroke and ischaemia),
XX cardiovascular diseases (e.g. atherosclerosis and myocardial infarction),
XX immunological diseases (e.g. platelet disorder) and embryonic liver
XX disorders. Preferably they are used to prevent acute cardiac ischaemia
XX following angioplasty and metastatic cancers, especially of the colon and
XX liver
XX
XX Sequence 47 AA;
Query Match 20.6%; Score 268; DB 4; Length 47;
Best Local Similarity 100.0%; Pred. No. 7.3e-16;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 114 COTRYGFDQFALYKGGDPAPYKNPWRWYRASFPFIITVTAHSGTYRC 160
Db 1 COTRYGFDQFALYKGGDPAPYKNPWRWYRASFPFIITVTAHSGTYRC 47
RESULT 12
ABU11225
ID ABU11225 standard; peptide; 47 AA.
XX
XX ABU11225;
XX
XX 06-FEB-2003 (first entry)
XX
```

	Human TANGO 268 IgG like domain #2.
DE	Human; mouse; variable heavy; VH; antigen; cancer;
KW	complementarity determining region; TANGO 268; glycoprotein VI; GPVI;
KW	TANGO 268; extracellular matrix; collagen; platelet release;
KW	proliferation; migration; embryogenesis; inflammation; thrombosis;
KW	degranulation; thrombocytopenia; antibody; thrombotic disorder;
KW	cerebral vascular disease; stroke; ischaemia; venous thromboembolism;
KW	leg swelling; pain; ulceration; pulmonary embolism; coronary disease;
KW	cardiovascular disease; angina pectoris; myocardial infarction;
KW	coronary restenosis; atherosclerosis; immunological disorder;
KW	developmental disorder; embryonic disorder; liver disorder;
KW	cerebral vascular disease; venous thromboembolism disease.
OS	Homo sapiens.
XX	
PN	WO200280968-A1.
XX	
PD	17-OCT-2002.
XX	
XX	09-APR-2002; 2002WO-US011122.
XX	
PR	09-APR-2001; 2001US-00829495.
XX	
PA	(MILL-) MILLENNIUM PHARM INC.
XX	
PI	Busfield SJ, Villevall J, Jandrot-Perrus M, Vainchenker W;
PI	Gill DS, Qian DM, Kingsbury G;
DR	WPI; 2003-058477/05.
XX	
PT	Novel substantially purified antibody immunospecifically binding to TANGO
PT	268 antigen, useful for treating bleeding disorders such as
PT	thrombocytopenia, stroke, ischemia, pulmonary embolism, atherosclerosis.
XX	
PS	Disclosure; Page 212; 236pp; English.
XX	
CC	This invention relates to a novel purified antibody comprising a variable
CC	heavy (VH) complementarity determining region (CDR)1, VH CDR2 or VH CDR3;
CC	or variable light (VL) CDRI, VL CDR2 or VL CDR3, and immunospecifically
CC	binding to a TANGO 268 (also referred as glycoprotein VI (GPVI)) antigen.
CC	The antibodies of the invention act to decrease or block TANGO 268
CC	binding to extracellular matrix components, or as a Collagen or platelet
CC	release and aggregation blocker. The antibodies of the invention are
CC	useful for modulating proliferation, migration, morphology,
CC	differentiation and/or function of megakaryocytes and platelets,
CC	including during development e.g. embryogenesis, modulating leukocyte-
CC	platelet and platelet-endothelium interactions in inflammation and/or
CC	thrombosis, and modulating platelet aggregation and degranulation. They
CC	are also useful for modulating disorders associated with abnormal or
CC	aberrant megakaryocyte and/or platelet proliferation, migration,
CC	morphology, differentiation and/or function, e.g. bleeding disorders such
CC	as thrombocytopenia. Other diseases which may be modulated by these
CC	antibodies are thrombotic disorders, cerebral vascular diseases (e.g.
CC	stroke and ischaemia) venous thromboembolism diseases (e.g. diseases
CC	involving leg swelling, pain and ulceration, pulmonary embolism, etc);
CC	coronary diseases (e.g. cardiovascular diseases including angina
CC	pectoris, myocardial infarction, coronary restenosis, atherosclerosis,
CC	etc); immunological disorders, developmental disorders, embryonic
CC	disorders, liver disorders, cerebral vascular diseases, venous
CC	thromboembolism disease, coronary diseases, and metastatic cancers. The
CC	antibodies of the invention only causes a transient decrease in platelet
CC	counts, platelet aggregation, and/or platelet activation and so have some
CC	advantages over prior art methods. The present sequence represents a
CC	peptide sequence used to generate the antibodies of the invention
XX	
SQ	Sequence 47 AA;
	Query Match 20.6%; Score 268; DB 6; Length 47;
	Best Local Similarity 100.0%; Pred.No. 7.3e-16; Indels 0; Gaps 0
	Matches 47; Conservative 0; Mismatches 0;
QY	114 COTRYGFDQFALYKEGDPAKYKNPWRMYRASFPFIITVAASHSGTYRC 160



Qy 172 SAPSDPL 178  
Db 177 SQRSEVL 183

RESULT 14  
AAO19233  
ID AAO19233 standard; protein; 145 AA.  
XX  
AC AAO19233;  
XX  
DT 27-NOV-2002 (first entry)  
XX  
DE Human putative inhibitory receptor SEQ ID NO: 29.  
XX  
KW Human; leukocyte immunoglobulin receptor-like protein; LIR-like protein;  
KW vulnary; neuroprotective; anti-inflammatory; cerebroprotective;  
KW nutritional supplement; lymphoid disorder; burn; wound; ulcer; stroke;  
KW Alzheimer's disease; amyotrophic lateral sclerosis; fibrosis; cancer;  
KW immune disorder; multiple sclerosis; allergy; inflammation; infertility;  
KW cytosstatic; immunosuppressive; anti-diabetic; antinfertility.  
XX  
OS Homo sapiens.  
XX  
FN WO2000266600-A2.  
XX  
PD 29-AUG-2002.  
XX  
PF 28-DEC-2001; 2001WO-US049435.  
XX  
PR 29-DEC-2000; 2000US-00751518.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Boyle BJ, Kuo C, Mize NK, Haley-Vicente DA, Arterburn MC;  
PI Tang YT, Zhou P, Liu C, Asundi V, Drmanac RT, Yeung G, Palencia S;  
XX  
DR WPI; 2002-674924/72.  
XX  
XX New leukocyte immunoglobulin receptor-like (LIR-like) polynucleotides and  
PT polypeptides, useful in research, as nutritional sources, or for treating  
PT wounds, Alzheimer's disease, inflammations, infertility, stroke or  
PT cancers.  
XX  
PS Example 5; Page 188-189; 215pp; English.  
XX  
CC The present invention provides the protein and coding sequences of human  
CC leukocyte immunoglobulin receptor-like molecules. These can be used as  
CC nutritional sources or supplements, or for treating myeloid or lymphoid  
CC disorders, burns, wounds, ulcers, Alzheimer's disease, amyotrophic  
CC lateral sclerosis, lung or liver fibrosis, immune disorders such as  
CC severe combined immunodeficiency, multiple sclerosis, allergies, graft-  
CC versus-host disease, inflammations, infertility, stroke, or cancers. The  
CC present sequence is a polypeptide described in the exemplification of the  
CC invention

Qy 1 QSGPLPKPSLQALPSLSVPLEKPVTLRCQPGVD---LYRLEKLS--SRQD---QAV 52  
Db 22 QAGHLPKPTLWAEPSGVIIQSGPVTLCQSLQAEYHLYRENKASWVRRIQEPKNGQ 81  
Qy 53 LPIPAKWSLAGRYCSYNGSLWPSQLBELVATGVFAKPSLSAQCPAVSSGGDVTL 112  
Db 82 FPIPSITWEHAGRYHCQYSHNSHSYSYDPLELVVTGAYSKPTLSALPSFVVTGNGVTL 141  
Qy 113 QC 114  
Db 142 QC 143

RESULT 15  
ABB42669  
ID ABB42669 standard; peptide; 100 AA.  
XX  
AC ABB42669;  
XX  
DT 04-FEB-2002 (first entry)  
XX  
DE Peptide #10175 encoded by human foetal liver single exon probe.  
XX  
KW Human; foetal liver; gene expression; single exon nucleic acid probe.  
XX  
OS Homo sapiens.  
XX  
FN WO200157277-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 30-JAN-2001; 2001WO-US000669.  
XX  
PR 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
DR WPI; 2001-483447/52.  
XX  
PT Human genome-derived single exon nucleic acid probes useful for analyzing  
PT gene expression in human fetal liver.  
XX  
PS Claim 27; SEQ ID NO 35304; 639pp + Sequence Listing; English.  
XX  
CC The invention relates to a single exon nucleic acid probe for measuring  
CC human gene expression in a sample derived from human foetal liver. The  
CC single exon nucleic acid probes may be used for predicting, measuring and  
CC displaying gene expression in samples derived from human fetal liver. The  
CC present sequence is a peptide encoded by a single exon nucleic acid probe  
CC of the invention. Note: The sequence data for this patent did not form  
CC part of the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 100 AA;  
Query Match 17.4%; Score 227.5; DB 4; Length 100;  
Best Local Similarity 50.0%; Pred. No. 6.5e-12;  
Matches 50; Conservative 16; Mismatches 25; Indels 9; Gaps 3;  
Qy 91 FAKPSLSAQCPAVSSGGDVTLCQTRYGFQFALYKEG---DP---APYKNPERWYRA 143  
Db 3 YDRVSLSVQPGFTVASGENVTLLCQSQGMOTFLTKEGAADDPWRLRSTTQSQK--YQA 60  
Qy 144 SFPIITVTAAHSGTVRCYCSFSSRDPFLWSAPSDPLELVVT 183  
Db 61 EPPMGFVTSAHAGTYRCYCSQSSKPYLLTHPSDFPLELVVS 100

RESULT 16  
AAM36482  
ID AAM36482 standard; protein; 100 AA.  
XX  
AC AAM36482;  
XX  
DT 17-OCT-2001 (first entry)  
XX



PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
XX WPI; 2001-488900/53.  
XX Human genome-derived single exon nucleic acid probes useful for analyzing  
PT gene expression in human bone marrow.  
XX Example 4; SEQ ID NO 36680; 658pp + Sequence Listing; English.  
XX The present invention provides a number of single exon nucleic acid  
CC probes which are derived from genomic sequences expressed in the human  
CC bone marrow. They can be used to measure gene expression in bone marrow  
CC samples, which may enable the improved diagnosis and treatment of cancers  
CC such as lymphoma, leukaemia and myeloma. The present sequence is a  
CC protein encoded by one of the probes of the invention  
XX Sequence 100 AA;  
SQ  
Query Match 17.4%; Score 227.5; DB 4; Length 100;  
Best Local Similarity 50.0%; Pred. No. 6.5e-12;  
Matches 50; Conservative 16; Mismatches 25; Indels 9; Gaps 3;  
QY 91 FAKPSLSAQPAPVSSGGDVTLCQCTRYGDFQFALYKEG---DP---APYKNPERWYRA 143  
DB 3 YDRVSLSVQPGPTVAGSGENVTLLCQSGWMQTFLTKGGAADDPWRLRSTYQSQK--YQA 60  
QY 144 SPPIITVTAHSGTYRCYFSFSDPFLYMSAPSDPLELVVT 183  
DB 61 EFPMPGPTSAHAGTYRCYGSQSOSKPYLLTHPSDPLELVVS 100  
RESULT 19  
AAM63559  
ID AAM63559 standard; protein; 100 AA.  
XX AAM63559;  
AC AAM63559;  
DT 05-NOV-2001 (first entry)  
XX Human brain expressed single exon probe encoded protein SEQ ID NO: 35664.  
DE Human; brain expressed exon; gene expression analysis; probe; microarray;  
KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.  
XX Homo sapiens.  
XX WO200157275-A2.  
FN 09-AUG-2001.  
PD 30-JAN-2001; 2001WO-US000667.  
PF 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
XX WPI; 2001-483446/52.

XX Single exon nucleic acid probes for analyzing gene expression in human  
PT brains.  
XX Example 4; SEQ ID NO 35664; 650pp + Sequence Listing; English.  
XX The present invention provides a number of single exon nucleic acid  
CC probes which are derived from genomic sequences expressed in the human  
CC brain. They can be used to measure gene expression in brain cell samples,  
CC which may enable the diagnosis and improved treatment of nervous system  
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, f  
CC epilepsy and cancers. The present sequence is a protein encoded by one of  
CC the probes of the invention  
XX Sequence 100 AA;  
SQ  
Query Match 17.4%; Score 227.5; DB 4; Length 100;  
Best Local Similarity 50.0%; Pred. No. 6.5e-12;  
Matches 50; Conservative 16; Mismatches 25; Indels 9; Gaps 3;  
QY 91 FAKPSLSAQPAPVSSGGDVTLCQCTRYGDFQFALYKEG---DP---APYKNPERWYRA 143  
DB 3 YDRVSLSVQPGPTVAGSGENVTLLCQSGWMQTFLTKGGAADDPWRLRSTYQSQK--YQA 60  
QY 144 SPPIITVTAHSGTYRCYFSFSDPFLYMSAPSDPLELVVT 183  
DB 61 EFPMPGPTSAHAGTYRCYGSQSOSKPYLLTHPSDPLELVVS 100  
RESULT 20  
ABG58080  
ID ABG58080 standard; peptide; 100 AA.  
XX ABG58080;  
AC ABG58080;  
DT 25-FEB-2003 (first entry)  
XX Human liver peptide, SEQ ID No 36728.  
DE Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;  
KW hypercholesterolaemia; coronary heart disease.  
XX Homo sapiens.  
XX WO200157273-A2.  
FN 09-AUG-2001.  
PD 30-JAN-2001; 2001WO-US000664.  
PF 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
XX WPI; 2001-488898/53.  
XX Human genome-derived single exon nucleic acid probes useful for analyzing  
PT gene expression in human adult liver.  
XX Claim 27; SEQ ID NO 36728; 658pp; English.  
XX The invention relates to a single exon nucleic acid probe (SENP) (I) for  
CC measuring human gene expression in a sample derived from human adult  
CC liver, comprising one of 13109 defined nucleotide sequences given in the  
CC specification (or complements/ fragments). The probe hybridises at high

CC stringency to a nucleic acid molecule expressed in the human adult liver.  
CC (1) may be used for predicting, measuring and displaying gene expression  
CC in samples derived from human adult liver. The genes identified may be  
CC involved in genetic liver diseases such as cirrhosis,  
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is  
CC associated with coronary heart disease. ABG47348-ABG59930 represent human  
CC liver single exon encoded peptides of the invention. Note: The sequence  
CC information for this patent does not appear in the printed specification  
CC but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 100 AA;

Query Match 17.4%; Score 227.5; DB 4; Length 100;  
Best Local Similarity 50.0%; Pred. No. 6.5e-12;  
Matches 50; Conservative 16; Mismatches 25; Indels 9; Gaps 3;  
QY 91 FAKPSLSAQPGPAVSSGGDVTLLCQCYRGDFQFALYKEG---DP---APYKNERWYRA 143  
DB 3 YDRVSLSVQPGPTVASEGNTVLLCQSQGWMTFLLTKEGAADDPWRLRSTYQSK--YQA 60  
QY 144 SFPITVTAAHSGTYRCYCSFSSRDPYLSAPSDPLELVVT 183  
DB 61 EFPMPVPTSAHAGTYRCYCSQSSKPYLLTHPSDPLELVVS 100

RESULT 21  
ABG45662  
ID ABG45662 standard; peptide; 100 AA.  
AC ABG45662;  
DT 19-AUG-2002 (first entry)  
DE Human peptide encoded by genome-derived single exon probe SEQ ID 35327.  
KW Human; single exon probe; asthma; lung cancer; COPD; ILD;  
KW chronic obstructive pulmonary disease; interstitial lung disease;  
KW familial idiopathic pulmonary fibrosis; neurofibromatosis;  
KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;  
KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;  
KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;  
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;  
KW primary ciliary dyskinesia; pulmonary hypertension;  
KW hyaline membrane disease.

XX Homo sapiens.  
XX WO200186003-A2.  
XX 15-NOV-2001.  
XX 30-JAN-2001; 2001WO-US000665.  
XX 04-FEB-2000; 2000US-0180312P.  
XX 26-MAY-2000; 2000US-0207456P.  
XX 30-JUN-2000; 2000US-00608408.  
XX 03-AUG-2000; 2000US-00632366.  
XX 21-SEP-2000; 2000US-0234687P.  
XX 27-SEP-2000; 2000US-0236359P.  
XX 04-OCT-2000; 2000GB-00024263.  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
PI WPI; 2002-114183/15.  
DR Spatially-addressable set of single exon nucleic acid probes, used to  
XX measure gene expression in human lung samples.  
XX  
XX Claim 27; SEQ ID NO 35327; 634pp; English.

CC The invention relates to a spatially-addressable set of single exon  
CC nucleic acid probes for measuring gene expression in a sample derived  
CC from human lung comprising single exon nucleic acid probes having one of  
CC 12614 nucleic acid sequences mentioned in the specification, or their  
CC complements or the 12387 open reading frames derived from the 12614  
CC probes. Also included are a microarray comprising the novel set of probes  
CC; the novel set of probes which hybridise at high stringency to a nucleic  
CC acid expressed in the human lung; measuring gene expression in a sample  
CC derived from human lung, comprising (a) contacting the array with a  
CC collection of detectably labeled nucleic acids derived from human lung  
CC mRNA, and (b) measuring the label detectably bound to each probe of the  
CC array; identifying exons in a eukaryotic genome, comprising (a)  
CC algorithmically predicting at least one exon from genomic sequences of  
CC the eukaryote; and (b) detecting specific hybridisation of detectably  
CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,  
CC having a fragment identical to the predicted exon, the probe is included  
CC in the above mentioned microarray; assigning exons to a single gene,  
CC comprising (a) identifying exons from genomic sequence by the method  
CC above and (b) measuring the expression of each of the exons in several  
CC tissues and/or cell types using hybridisation to a single exon  
CC microarrays having a probe with the exon, where a common pattern of  
CC expression of the exons in the tissues and/or cell types indicates that  
CC the exons should be assigned to a single gene; a peptide comprising one  
CC of 12011 sequences, mentioned in the specification, or encoded by the  
CC probes/open reading frames (ORF). The probes are used for gene expression  
CC analysis, and for identifying exons in a gene, particularly using human  
CC lung derived mRNA and for the study of lung diseases such as asthma, lung  
CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung  
CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,  
CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-  
CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary  
CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,  
CC Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary  
CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The  
CC present sequence is a peptide/protein encoded by a single exon probe of  
CC the invention. Note: The sequence data for this patent did not form part  
CC of the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 100 AA;

Query Match 17.4%; Score 227.5; DB 5; Length 100;  
Best Local Similarity 50.0%; Pred. No. 6.5e-12;  
Matches 50; Conservative 16; Mismatches 25; Indels 9; Gaps 3;  
QY 91 FAKPSLSAQPGPAVSSGGDVTLLCQCYRGDFQFALYKEG---DP---APYKNERWYRA 143  
DB 3 YDRVSLSVQPGPTVASEGNTVLLCQSQGWMTFLLTKEGAADDPWRLRSTYQSK--YQA 60  
QY 144 SFPITVTAAHSGTYRCYCSFSSRDPYLSAPSDPLELVVT 183  
DB 61 EFPMPVPTSAHAGTYRCYCSQSSKPYLLTHPSDPLELVVS 100

RESULT 22  
ABG61272  
ID AAB61272 standard; protein; 47 AA.  
XX AAB61272;  
XX 04-APR-2001 (first entry)  
XX Mouse TANGO 268 Ig-like domain #2.  
XX Mouse; TANGO 268; cardiant; cerebroprotective; cytosolic; anticonagulant;  
KW thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI;  
KW platelet membrane glycoprotein receptor; bleeding disorder;  
KW blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;  
KW ischaemia; cardiovascular disease; immunological disease; liver disorder;  
XX cancer.  
XX Mus musculus.  
XX

PN WO200100810-A1.  
 PD 04-JAN-2001.  
 PF 30-JUN-2000; 2000WO-US018152.  
 PR 30-JUN-1999; 99US-00345468.  
 PR 06-DEC-1999; 99US-00454824.  
 PR 14-FEB-2000; 2000US-00503387.  
 XX (MILL-) MILLENNIUM PHARM INC.  
 XX Busfield SJ, Villelval J, Jandrot-Perrus M, Vainchencker W;  
 PI Gill DS, Qian MD, Kingsbury G;  
 XX WPI; 2001-080877/09.  
 XX  
 PT New genes encoding human platelet-expressed collagen receptor,  
 PT glycoprotein VI, and its modulators, useful for preventing, treating and  
 PT diagnosing hemorrhagic disorders, thrombotic diseases and immunological  
 PT disorders.  
 XX  
 PS Disclosure; Page 210-211; 227pp; English.  
 XX  
 CC The present sequence is given in a specification relating to an isolated  
 CC nucleic acid molecule encoding a platelet membrane glycoprotein receptor  
 CC glycoprotein VI (GPVI), also called TANGO 268. The GPVI polynucleotides  
 CC and polypeptides and their modulators, e.g. antisense nucleic acids,  
 CC ribozymes and antibodies, are useful for preventing, treating and  
 CC diagnosing disorders associated with aberrant expression or activity of  
 CC GPVI. These disorders include bleeding disorders (e.g.  
 CC thrombocytopenia), blood vessel injury, thrombotic disorders (e.g.  
 CC thrombotic occlusion of the coronary arteries), haemorrhagic disorders,  
 CC coronary artery and cerebral artery diseases (e.g. stroke and ischaemia),  
 CC cardiovascular diseases (e.g. atherosclerosis and myocardial infarction),  
 CC immunological diseases (e.g. platelet disorder) and embryonic liver  
 CC disorders. Preferably they are used to prevent acute cardiac ischaemia  
 CC following angioplasty and metastatic cancers, especially of the colon and  
 CC liver  
 XX  
 SQ Sequence 47 AA;  
 Query Match 16.9%; Score 220; DB 4; Length 47;  
 Best Local Similarity 78.7%; Pred. No. 1.1e-11;  
 Matches 37; Conservative 4; Mismatches 6; Indels 0; Gaps 0;  
 QY 114 CQTRYGDFQFALYKGGDPAPYKNPERWYRASPIITVTAHSGTYRC 160  
 DB 1 COSPYSFDFVLYKGGDTGPKYKPKWYRANPFIITVTAHSGTYRC 47  
 RESULT 23  
 ABU11238  
 ID ABU11238 standard; peptide; 47 AA.  
 AC  
 XX ABU11238;  
 XX  
 DT 06-FEB-2003 (first entry)  
 XX  
 DE TANGO 268 IgG like domain #2.  
 XX  
 KW Human; mouse; variable heavy; VH; antigen; cancer;  
 KW complementarity determining region; TANGO 268; glycoprotein VI; GPVI;  
 KW TANGO 268; extracellular matrix; collagen; platelet release;  
 KW proliferation; migration; embryogenesis; inflammation; thrombosis;  
 KW degranulation; thrombocytopenia; antibody; thrombotic disorder;  
 KW cerebral vascular disease; stroke; ischaemia; venous thromboembolism;  
 KW leg swelling; pain; ulceration; pulmonary embolism; coronary disease;  
 KW cardiovascular disease; angina pectoris; myocardial infarction;  
 KW coronary restenosis; atherosclerosis; immunological disorder;  
 KW developmental disorder; embryonic disorder; liver disorder;  
 KW cerebral vascular disease; venous thromboembolism disease.

OS Mus musculus.  
 XX WO200280968-A1.  
 XX 17-OCT-2002.  
 XX 09-APR-2002; 2002WO-US011122.  
 XX 09-APR-2001; 2001US-00829495.  
 XX (MILL-) MILLENNIUM PHARM INC.  
 XX Busfield SJ, Villelval J, Jandrot-Perrus M, Vainchencker W;  
 PI Gill DS, Qian DM, Kingsbury G;  
 XX WPI; 2003-058477/05.  
 XX  
 PT Novel substantially purified antibody immunospecifically binding to TANGO  
 PT 268 antigen, useful for treating bleeding disorders such as  
 PT thrombocytopenia, stroke, ischemia, pulmonary embolism, atherosclerosis.  
 XX  
 PS Disclosure; Page 219; 236pp; English.  
 XX  
 CC This invention relates to a novel purified antibody comprising a variable  
 CC heavy (VH) complementarity determining region (CDR)1, VH CDR2 or VH CDR3;  
 CC or variable light (VL) CDR1, VL CDR2 or VL CDR3, and immunospecifically  
 CC binding to a TANGO 268 (also referred as glycoprotein VI (GPVI)) antigen.  
 CC The antibodies of the invention act to decrease or block TANGO 268  
 CC binding to extracellular matrix components, or as a Collagen or platelet  
 CC release and aggregation blocker. The antibodies of the invention are  
 CC useful for modulating proliferation, migration, morphology,  
 CC differentiation and/or function of megakaryocytes and platelets,  
 CC including during development e.g. embryogenesis, modulating leukocyte-  
 CC platelet and platelet-endothelium interactions in inflammation and/or  
 CC thrombosis, and modulating platelet aggregation and degranulation. They  
 CC are also useful for modulating disorders associated with abnormal or  
 CC aberrant megakaryocyte and/or platelet proliferation, migration,  
 CC morphology, differentiation and/or function, e.g. bleeding disorders such  
 CC as thrombocytopenia. Other diseases which may be modulated by these  
 CC antibodies are thrombotic disorders, cerebral vascular diseases (e.g. stroke  
 CC and ischaemia) venous thromboembolism diseases (e.g. diseases  
 CC involving leg swelling, pain and ulceration, pulmonary embolism, etc);  
 CC coronary diseases (e.g. cardiovascular diseases including angina  
 CC pectoris, myocardial infarction, coronary restenosis, atherosclerosis,  
 CC etc); immunological disorders, developmental disorders, embryonic  
 CC disorders, liver diseases, cerebral vascular diseases, venous  
 CC thromboembolism disease, coronary diseases, and metastatic cancers. The  
 CC antibodies of the invention only causes a transient decrease in platelet  
 CC counts, platelet aggregation, and/or platelet activation and so have some  
 CC advantages over prior art methods. The present sequence represents a  
 CC peptide sequence used to generate the antibodies of the invention  
 XX  
 SQ Sequence 47 AA;  
 Query Match 16.9%; Score 220; DB 6; Length 47;  
 Best Local Similarity 78.7%; Pred. No. 1.1e-11;  
 Matches 37; Conservative 4; Mismatches 6; Indels 0; Gaps 0;  
 QY 114 CQTRYGDFQFALYKGGDPAPYKNPERWYRASPIITVTAHSGTYRC 160  
 DB 1 COSPYSFDFVLYKGGDTGPKYKPKWYRANPFIITVTAHSGTYRC 47  
 RESULT 24  
 ADK98546  
 ID ADK98546 standard; protein; 221 AA.  
 XX  
 AC ADK98546;  
 XX  
 DT 03-JUN-2004 (first entry)  
 XX  
 DB Human immune response associated protein IRAP-9 protein.

KW immune response associated protein; IRAP; antiarteriosclerotic;  
KW cytosolic; neuroprotective; antiparkinsonian; hepatotropic;  
KW cerebroprotective; antiinflammatory; neurotropic; vasotropic;  
KW arteriosclerosis; cirrhosis; cancer; stroke; Alzheimer's disease;  
KW Parkinson's; Crohn's; gene therapy; human.  
XX Homo sapiens.  
XX  
XX WO2004020593-A2.  
XX  
XX 11-MAR-2004.  
XX  
XX 26-AUG-2003; 2003WO-US026988.  
XX  
XX 30-AUG-2002; 2002US-0407561P.  
XX 11-SEP-2002; 2002US-0410178P.  
XX 13-SEP-2002; 2002US-0410571P.  
XX 18-OCT-2002; 2002US-0419906P.  
XX 25-OCT-2002; 2002US-0421445P.  
XX  
XX (INCY-) INCYTE CORP.  
XX  
XX Ramkumar J, Swarnakar A, Elliott VS, Hafalia AJA, Richardson TW;  
XX Lee SY, Lindquist EA, Marquis JP, Chawla NK, Khare R, Becha SD;  
XX  
XX WPI; 2004-239178/22.  
XX N-PSDB; ADK98581.  
XX  
XX New isolated immune response associated proteins (IRAP) polypeptide and  
XX polynucleotide, useful for diagnosing and/or treating disorders with  
XX aberrant expression of IRAP, such as arteriosclerosis, cirrhosis, cancer  
XX and stroke.  
XX  
XX Claim 1; SEQ ID NO 9; 207pp; English.  
XX  
XX The invention relates to a novel isolated immune response associated  
XX protein (IRAP) comprising any of 35 fully defined sequences given in the  
XX specification. The polypeptide of the invention demonstrates  
XX antiarteriosclerotic, cytostatic, neuroprotective, antiparkinsonian,  
XX hepatotropic, cerebroprotective, antiinflammatory, neurotropic and  
XX vasotropic activities and may be useful for treating a disease or  
XX condition associated with decreased expression or overexpression of  
XX functional immune response associated proteins, while the antibody is  
XX useful for diagnosing a condition or disease associated with the  
XX expression of IRAP, such as arteriosclerosis, cirrhosis, cancer, stroke,  
XX Alzheimer's disease, Parkinson's disease and Crohn's disease.  
XX Furthermore, the molecules of the invention may be utilised during gene  
XX therapy procedures. The current sequence is that of a human IRAP protein  
XX of the invention.  
XX  
XX Sequence 221 AA;  
Query Match 16.8%; Score 218.5; DB 8; Length 221;  
Best Local Similarity 31.7%; Pred. No. 1.1e-10;  
Matches 60; Conservative 32; Mismatches 80; Indels 17; Gaps 3;  
Qy 1 QSGPLPKPSLQALPSSLVPLEKPYTLRCQPGGVLDYLRLEKLSRRYQD----- 49  
Db 22 QEGDFPMFFISAKSPVPLDGSVKIQCAIREAYLTQLMIIKNSTYREIGRLKFWNET 81  
Qy 50 QAVLFIPAMKESLAGRYCSQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGD 109  
Db 82 DPEVIDHMDANKAGRYQCQRIQHYRFRYSDDTLVELVTGLYKPFUSADRGVLMPGEN 141  
Qy 110 VTLCQCTRY-GFDQFALYKEGDPAPYKNPERWYRASPFIITVTAHSGTYRCYFSFSSRDP 168  
Db 142 ISLTCSSAHIPFDFSLAKEGELSIPQHQSGEHPANFSLGPDVLNVSGIYRLH-----PP 196  
Qy 169 YLMSAPSDP 177  
Db 197 RLHDAELDP 205

RESULT 25  
AAM15998  
ID AAM15998 standard; protein; 100 AA.  
XX  
XX AAM15998;  
XX  
XX 12-OCT-2001 (first entry)  
XX  
XX Peptide #2432 encoded by probe for measuring cervical gene expression.  
XX  
XX Probe; human; microarray; gene expression; cervical epithelial cell;  
XX cervical cancer.  
XX  
XX Homo sapiens.  
XX  
XX WO200157278-A2.  
XX  
XX 09-AUG-2001.  
XX  
XX 30-JAN-2001; 2001WO-US000670.  
XX  
XX 04-FEB-2000; 2000US-0180312P.  
XX 26-MAY-2000; 2000US-0207456P.  
XX 30-JUN-2000; 2000US-00608408.  
XX 03-AUG-2000; 2000US-00632366.  
XX 21-SEP-2000; 2000US-0234587P.  
XX 27-SEP-2000; 2000US-0236359P.  
XX 04-OCT-2000; 2000GB-00024263.  
XX  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
XX WPI; 2001-488901/53.  
XX  
XX Human genome-derived single exon nucleic acid probes useful for analyzing  
XX gene expression in human cervical epithelial cells.  
XX  
XX Claim 27; SEQ ID NO 20824; 487pp; English.  
XX  
XX The present invention relates to human single exon nucleic acid probes  
XX (SENPs; see AAI10068-AAI28459). The present sequence is a peptide encoded  
XX by one such probe. The SENPs are derived from human HeLa cells. The SENPs  
XX can be used to produce a single exon microarray, which can be used for  
XX measuring human gene expression in a sample derived from human cervical  
XX epithelial cells. By measuring gene expression, the probes are therefore  
XX useful in grading and/or staging of diseases of the cervix, notably  
XX cervical cancer. Note: The sequence data for this patent did not form  
XX part of the printed specification, but was obtained in electronic format  
XX directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 100 AA;  
Query Match 16.6%; Score 216.5; DB 4; Length 100;  
Best Local Similarity 50.0%; Pred. No. 5.9e-11;  
Matches 49; Conservative 13; Mismatches 31; Indels 5; Gaps 1;  
Qy 91 FAKPSLSAQPGPAVSSGDDVTLCQCTRYGFDQFALYKEGDPAP-----YKNPERWYRASF 145  
Db 3 YDRPSSLVSQVPVTPVAPGKNVTLLCQSRGQFHTTLLTKEGAGHPPLHLRSHQAQQOAEF 62  
Qy 146 PIITVTAHSGTYRCYFSFSSRDPYLMASPSDPLELVVT 183  
Db 63 RMGFVTSAHVGTYRCYSSLSNPNYLLSLPSDPLELVVS 100  
Search completed: October 29, 2005, 03:43:59  
Job time : 175 secs







;; PRIOR FILING DATE: 2000-06-30  
;; PRIOR APPLICATION NUMBER: 09/503,387  
;; PRIOR FILING DATE: 2000-02-14  
;; PRIOR APPLICATION NUMBER: 09/454,824  
;; PRIOR FILING DATE: 1999-12-06  
;; PRIOR APPLICATION NUMBER: 09/345,468  
;; PRIOR FILING DATE: 1999-06-30  
;; NUMBER OF SEQ ID NOS: 78  
;; SOFTWARE: FastSeq for Windows Version 3.0  
;; SEQ ID NO 9  
;; LENGTH: 249  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-850-034-9

Query Match 100.0%; Score 1304; DB 16; Length 249;  
Best Local Similarity 100.0%; Pred. No. 9.7e-96;  
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRLEKLSRRYQDQAVLFIPIAMKR 60  
Db 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRLEKLSRRYQDQAVLFIPIAMKR 60

Qy 61 SLAGYRCSYONGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLCQTRYGF 120  
Db 61 SLAGYRCSYONGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLCQTRYGF 120

Qy 121 DQFALYKEGDPAPYKPNRWYRASPIITVTAHSGTYRCYFSGSRDPYLSAPSDPLEL 180  
Db 121 DQFALYKEGDPAPYKPNRWYRASPIITVTAHSGTYRCYFSGSRDPYLSAPSDPLEL 180

Qy 181 VVTGTSVTPSRILPTPPSSVAEFSEATAELTVSFNKNVFTTTSRITTSKESDSPAGP 240  
Db 181 VVTGTSVTPSRILPTPPSSVAEFSEATAELTVSFNKNVFTTTSRITTSKESDSPAGP 240

Qy 241 ARQYTKGN 249  
Db 241 ARQYTKGN 249

RESULT 4  
US-10-333-481-13  
;; Sequence 13, Application US/10333481  
;; Publication No. US20040072256A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Ofer Mandelboim  
;; TITLE OF INVENTION: NK CELLS ACTIVATING RECEPTORS AND THEIR THERAPEUTIC AND DIAGNOSTIC  
;; FILE REFERENCE: 68657  
;; CURRENT APPLICATION NUMBER: US/10/333,481  
;; CURRENT FILING DATE: 2003-08-04  
;; PRIOR APPLICATION NUMBER: PCT/IL01/00664  
;; PRIOR FILING DATE: 2001-07-19  
;; NUMBER OF SEQ ID NOS: 26  
;; SOFTWARE: Patent in Ver. 2.1  
;; SEQ ID NO 13  
;; LENGTH: 237  
;; TYPE: PRT  
;; ORGANISM: homo sapiens  
US-10-333-481-13

Query Match 27.3%; Score 355.5; DB 15; Length 237;  
Best Local Similarity 38.4%; Pred. No. 3.1e-20;  
Matches 81; Conservative 30; Mismatches 77; Indels 23; Gaps 3;

Qy 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRL-----EKLSSS 45  
Db 22 QOQTLPPFIWAEPPHFMVPEKQVITCCQNGTGVAYEQLHFEGSLFAVDRPKPPRINKY 81

Qy 46 RYQDQAVLFIPIAMKRSLAGYRCSYONGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVS 105  
Db 82 KP-----YIPDNSEMAQYSCIYRVGELWSEPSNLLDLVVTMYDTTSLVHGPPEVI 135

Qy 106 SGGDVTLCQTRYGFDQFALYKEGDPAPYKPNRWYRASPIITVTAHSGTYRCYFSS 165  
Db 136 SGEKVFYFCHLDATATSMFLLLKEGRSSHVGKGVQAEEFPLGVTTHRGTYRC--FGS 193

Qy 166 RDPYLSAPSDPLELVVTVGTSTVTPSRILPTEP 196  
Db 194 YNNHANSFPSEPVKLLVTGDIENSTSLAPEDP 224

RESULT 5  
US-10-450-763-40516  
;; Sequence 40516, Application US/10450763  
;; Publication No. US20050196754A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Hyseq, Inc  
;; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
;; FILE REFERENCE: 790CIP3/US  
;; CURRENT APPLICATION NUMBER: US/10/450,763  
;; CURRENT FILING DATE: 2003-06-11  
;; PRIOR APPLICATION NUMBER: PCT/US01/08631  
;; PRIOR FILING DATE: 2001-03-30  
;; PRIOR APPLICATION NUMBER: 09/540,217  
;; PRIOR FILING DATE: 2000-03-31  
;; PRIOR APPLICATION NUMBER: 09/649,167  
;; PRIOR FILING DATE: 2000-08-23  
;; NUMBER OF SEQ ID NOS: 60736  
;; SOFTWARE: Custom  
;; SEQ ID NO 40516  
;; LENGTH: 170  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: DOMAIN  
;; LOCATION: (3)...(39)  
;; OTHER INFORMATION: RECEPTOR CELL NK GLYCOPROTEIN IMMUNOGLOB domain identified by  
;; OTHER INFORMATION: eMATRIX, accession number PD01652A, p-value=1.000e-40, raw score  
;; OTHER INFORMATION: of 15.35  
;; FEATURE:  
;; NAME/KEY: DOMAIN  
;; LOCATION: (42)...(147)  
;; OTHER INFORMATION: Immunoglobulin domain identified by PFam, accession name ig,  
;; OTHER INFORMATION: E-value=3.9e-05, PFam score of 21.6  
US-10-450-763-40516

Query Match 21.4%; Score 279.5; DB 18; Length 170;  
Best Local Similarity 37.7%; Pred. No. 2.3e-14;  
Matches 72; Conservative 22; Mismatches 56; Indels 41; Gaps 7;

Qy 7 KPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRLEKLSRRYQDQAVLFIPIAMKRSLAGRY 66  
Db 7 KPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRLEKLSRRYQDQAVLFIPIAMKRSLAGRY 66

Qy 67 RC-----SYONGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLCQTRYG 119  
Db 46 RCYGSVPHPSPYQ---LSAPSDPLDMVILIGLYEKPSLSAQPGPTVQAGENTLSCSSRSS 101

Qy 120 FDQFALYKEGDPAPYKPN-----ERWYRASPIITVTAHSGTYRCYFSSRD--PYLWSA 173  
Db 102 YDMYHLRSREGEAHERRLPAVRSLNGTFOADPFL--GPATHGTYRCFG-SFRDAPYENSN 158

Qy 174 PSDPLELVVTG 184  
Db 159 SSDPLLVSVTG 169

RESULT 6  
US-10-446-826-2  
;; Sequence 2, Application US/10446826  
;; Publication No. US20030186685A1  
;; GENERAL INFORMATION:  
;; APPLICANT: TANDON, NARENDRA N.  
;; APPLICANT: SUN, BING  
;; APPLICANT: NAKAMURA, TAKASHI

Sequence 2, Application 001/101-100

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Db 1 CQTRYGDFQFALYKEGDPAPYKNPERWYRASFPFIITVTAHSGTYRC 47
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RESULT 10
US-09-832-312-7
; Sequence 7, Application US/09832312
; Patent No. US20010049829A1
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-312-7
Query Match 20.6%; Score 268; DB 9; Length 47;
Best Local Similarity 100.0%; Pred. No. 3.9e-14;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 114 CQTRYGDFQFALYKEGDPAPYKNPERWYRASFPFIITVTAHSGTYRC 160
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Db 1 CQTRYGDFQFALYKEGDPAPYKNPERWYRASFPFIITVTAHSGTYRC 47
|||||

RESULT 11
US-09-829-495-7
; Sequence 7, Application US/09829495
; Publication No. US20040001826A1
; GENERAL INFORMATION:
; APPLICANT: Busfield SJ
; APPLICANT: Villevial J
; APPLICANT: Jandrot-Perrus M
; APPLICANT: Vainchenker W
; APPLICANT: Gill DS
; APPLICANT: Qian MD
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/829,495
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-829-495-7
Query Match 20.6%; Score 268; DB 11; Length 47;
Best Local Similarity 100.0%; Pred. No. 3.9e-14;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 114 CQTRYGDFQFALYKEGDPAPYKNPERWYRASFPFIITVTAHSGTYRC 160
|||||
Db 1 CQTRYGDFQFALYKEGDPAPYKNPERWYRASFPFIITVTAHSGTYRC 47
|||||

RESULT 12
US-10-850-034-7
; Sequence 7, Application US/10850034
; Publication No. US20040253236A1
; GENERAL INFORMATION:
; APPLICANT: Busfield SJ
; APPLICANT: Villevial J
; APPLICANT: Jandrot-Perrus M
; APPLICANT: Vainchenker W
; APPLICANT: Gill DS
; APPLICANT: Qian MD
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/10/850,034
; CURRENT FILING DATE: 2004-05-20
; PRIOR APPLICATION NUMBER: US/09/829,495
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-850-034-7
Query Match 20.6%; Score 268; DB 16; Length 47;
Best Local Similarity 100.0%; Pred. No. 3.9e-14;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 114 CQTRYGDFQFALYKEGDPAPYKNPERWYRASFPFIITVTAHSGTYRC 160
|||||
Db 1 CQTRYGDFQFALYKEGDPAPYKNPERWYRASFPFIITVTAHSGTYRC 47
|||||

RESULT 13
US-09-864-761-41304
; Sequence 41304, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecmica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
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2.

FILE REFERENCE: A60MICA-A-1	
CURRENT APPLICATION NUMBER: US 09/864,761	
CURRENT FILING DATE: 2001-05-23	
PRIOR APPLICATION NUMBER: US 60/180,312	
PRIOR FILING DATE: 2000-02-04	
PRIOR APPLICATION NUMBER: US 60/207,456	
PRIOR FILING DATE: 2000-05-26	
PRIOR APPLICATION NUMBER: US 09/632,366	
PRIOR FILING DATE: 2000-08-03	
PRIOR APPLICATION NUMBER: GB 24563.6	
PRIOR FILING DATE: 2000-10-04	
PRIOR APPLICATION NUMBER: US 60/236,359	
PRIOR FILING DATE: 2000-09-27	
PRIOR APPLICATION NUMBER: PCT/US01/00666	
PRIOR FILING DATE: 2001-01-30	
PRIOR APPLICATION NUMBER: PCT/US01/00667	
PRIOR FILING DATE: 2001-01-30	
PRIOR APPLICATION NUMBER: PCT/US01/00664	
PRIOR FILING DATE: 2001-01-30	
PRIOR APPLICATION NUMBER: PCT/US01/00669	
PRIOR FILING DATE: 2001-01-30	
PRIOR APPLICATION NUMBER: PCT/US01/00665	
PRIOR FILING DATE: 2001-01-30	
PRIOR APPLICATION NUMBER: PCT/US01/00668	
PRIOR FILING DATE: 2001-01-30	
PRIOR APPLICATION NUMBER: PCT/US01/00663	
PRIOR FILING DATE: 2001-01-30	
PRIOR APPLICATION NUMBER: PCT/US01/00662	
PRIOR FILING DATE: 2001-01-30	
PRIOR APPLICATION NUMBER: PCT/US01/00661	
PRIOR FILING DATE: 2001-01-30	
PRIOR APPLICATION NUMBER: PCT/US01/00670	
PRIOR FILING DATE: 2001-01-30	
PRIOR APPLICATION NUMBER: US 60/234,687	
PRIOR FILING DATE: 2000-09-21	
PRIOR APPLICATION NUMBER: US 09/608,408	

RESULT 18

US-09-864-761-36185

Sequence 36185, Application US/09864761

Patent No. US20020048763A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEI

FILE REFERENCE: Aeonica-X-1

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 2000-02-04

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 09/632,366

PRIOR FILING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: GB 24263.6

PRIOR FILING DATE: 2000-10-04

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00668

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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 36185
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC009892.2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 9.3
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 12
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 8.6
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 7.6
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 7.6
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 11
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 9.6
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 10
; OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 8.4
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 7.9
; OTHER INFORMATION: SWISSPROT HIT: P43626, EVALUE 2.00e-11
; OTHER INFORMATION: EST_HUMAN HIT: AU120189.1, EVALUE 2.00e-25
US-09-864-761-36185

Query Match      16.6%; Score 216.5; DB 9; Length 100;
Best Local Similarity 50.0%; Pred. No. 1.3e-09;
Matches 49; Conservative 13; Mismatches 31; Indels 5; Gaps 1;

Qy      91  FAKPSLQAQGPAYSSGGDVTLCQCTRYGDFQFALYKRGDPAP-----YKNPERWYRASF 145
Db      3  YDRSLSVQVPVTVPAGKNTLLCQSGQFTFTLLTGAGHPPLHLRSEHQAOQNAEP 62
Qy      146 PIITVTAHSGTYRCYCSFSSRDPYLMASPSDPLELVVT 183
Db      63  RMGPVTAHVGYTCYCSLSNSNPLYLLSPSDPLELVVS 100

RESULT 19
US-09-832-312-6
; Sequence 6, Application US/09832312
; Patent No. US20010049829A1
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Homo sapiens

Query Match      16.6%; Score 216; DB 11; Length 41;
Best Local Similarity 100.0%; Pred. No. 4.6e-10;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      28  CQGPFGVDLYRLEKLSRSSRYQDQAVLFIPAMKSLAGRYRC 68
Db      1  CQGPFGVDLYRLEKLSRSSRYQDQAVLFIPAMKSLAGRYRC 41

RESULT 21
US-10-850-034-6
; Sequence 6, Application US/10850034
; Publication No. US20040253236A1
; GENERAL INFORMATION:
; APPLICANT: Busfield SJ
; APPLICANT: Villevall J
; APPLICANT: Jandrot-Perrus M
; APPLICANT: Vainchenker W
; APPLICANT: Gill DS
; APPLICANT: Qian MD
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/10/850,034
; CURRENT FILING DATE: 2004-05-20
; PRIOR APPLICATION NUMBER: US/09/829,495
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
```

```
; ORGANISM: Homo sapiens
US-09-832-312-6

Query Match      16.6%; Score 216; DB 9; Length 41;
Best Local Similarity 100.0%; Pred. No. 4.6e-10;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      28  CQGPFGVDLYRLEKLSRSSRYQDQAVLFIPAMKSLAGRYRC 68
Db      1  CQGPFGVDLYRLEKLSRSSRYQDQAVLFIPAMKSLAGRYRC 41

RESULT 20
US-09-829-495-6
; Sequence 6, Application US/09829495
; Publication No. US20040001826A1
; GENERAL INFORMATION:
; APPLICANT: Busfield SJ
; APPLICANT: Villevall J
; APPLICANT: Jandrot-Perrus M
; APPLICANT: Vainchenker W
; APPLICANT: Gill DS
; APPLICANT: Qian MD
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/829,495
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Homo sapiens

Query Match      16.6%; Score 216; DB 11; Length 41;
Best Local Similarity 100.0%; Pred. No. 4.6e-10;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      28  CQGPFGVDLYRLEKLSRSSRYQDQAVLFIPAMKSLAGRYRC 68
Db      1  CQGPFGVDLYRLEKLSRSSRYQDQAVLFIPAMKSLAGRYRC 41

RESULT 21
US-10-850-034-6
; Sequence 6, Application US/10850034
; Publication No. US20040253236A1
; GENERAL INFORMATION:
; APPLICANT: Busfield SJ
; APPLICANT: Villevall J
; APPLICANT: Jandrot-Perrus M
; APPLICANT: Vainchenker W
; APPLICANT: Gill DS
; APPLICANT: Qian MD
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/10/850,034
; CURRENT FILING DATE: 2004-05-20
; PRIOR APPLICATION NUMBER: US/09/829,495
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
```







US-09-864-761-45373

Best Local Matches	Similarity	Ident. No.	Indels	Gaps
48	50.38	31	5	2

6 PALSVP0GPKVAGSENVTLLCSNWHOIDTFEFLTEGAHHPCLCKSKYQSYRHH0EFSMS 65

db 66 PVTSAOGGTYRCYSAIRSYPYLLSSPSYPQELVWS 100

Job time : 167 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 29, 2005, 03:37:27 ; Search time 39 Seconds

(without alignments)  
614.307 Million cell updates/sec

Title: US-09-503-387-3\_COPY\_21\_269

Perfect score: 1304

Sequence: 1 QSGPLPKESLQALPSSLVPL.....SPKESDSPAGPARQYTKGN 249

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 129754

Minimum DB seq length: 0

Maximum DB seq length: 250

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR 79:\*\*

1: PIR1:\*\*

2: PIR2:\*\*

3: PIR3:\*\*

4: PIR4:\*\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	305	23.4	239	2	G02630
2	145	11.1	237	2	A42013
3	141.5	10.9	184	2	T46433
4	88.5	6.8	189	2	G70512
5	88.5	6.8	233	2	G29577
6	88.5	6.8	235	2	S20000
7	88.5	6.8	246	2	PC4397
8	87	6.7	236	2	PC4396
9	86	6.6	233	1	JU0284
10	82.5	6.3	148	2	D71549
11	79.5	6.1	155	2	G72548
12	79.5	6.1	243	2	AC3600
13	79	6.1	213	2	A21177
14	78.5	6.0	136	2	JQ0473
15	78	6.0	206	2	A40305
16	78	6.0	238	2	T40820
17	76.5	5.9	138	2	E75509
18	76.5	5.9	233	2	JH0372
19	75.5	5.8	178	2	S29594
20	75.5	5.8	216	2	I51920
21	75.5	5.8	226	2	JQ1263
22	75.5	5.8	230	2	A56210
23	75.5	5.8	233	2	A86344
24	75	5.8	235	2	PC2022
25	75	5.8	243	2	S25755
26	74.5	5.7	235	2	S25058
27	74	5.7	183	2	A28335
28	74	5.7	241	2	D43273
29	73.5	5.6	186	2	H97920

30	73.5	5.6	186	2	D95050
31	73.5	5.6	243	2	B41710
32	73	5.6	85	2	B35690
33	73	5.6	136	2	S16848
34	73	5.6	166	2	A33402
35	73	5.6	182	2	I83053
36	73	5.6	201	1	WMBEHL
37	73	5.6	235	2	S14675
38	72.5	5.6	210	2	JC4122
39	72.5	5.6	215	2	B48463
40	72.5	5.6	244	2	T12458
41	72	5.5	182	2	A34647
42	72	5.5	212	2	PN0565
43	72	5.5	229	2	H83425
44	72	5.5	239	2	T45806
45	72	5.5	241	2	S32359
46	71.5	5.5	148	2	S35788
47	71.5	5.5	194	2	E95375
48	71.5	5.5	232	2	S17399
49	71.5	5.5	239	2	T45806
50	71	5.4	160	2	I47163
51	71	5.4	206	2	A75493
52	71	5.4	215	2	T23195
53	71	5.4	230	2	S49449
54	71	5.4	240	2	A39016
55	70.5	5.4	109	1	KVRB37
56	70.5	5.4	201	2	A97776
57	70.5	5.4	245	2	S19018
58	70	5.4	119	2	S30526
59	70	5.4	136	2	S42610
60	70	5.4	204	2	S22639
61	70	5.4	235	2	S25758
62	69.5	5.3	215	2	A48463
63	69	5.3	152	2	B26471
64	69	5.3	153	2	F96725
65	69	5.3	160	2	A72541
66	69	5.3	206	2	T23852
67	69	5.3	240	2	S01299
68	68.5	5.3	179	2	S34345
69	68.5	5.3	221	2	S49220
70	68.5	5.3	242	2	S06942
71	68.5	5.3	248	2	AH0472
72	68	5.2	139	2	S36325
73	68	5.2	212	2	C33258
74	68	5.2	240	2	A36791
75	67.5	5.2	104	2	I47165
76	67.5	5.2	116	2	F30517
77	67.5	5.2	128	2	A35690
78	67.5	5.2	238	2	S66358
79	67.5	5.2	240	2	A41797
80	67	5.1	140	2	I76667
81	67	5.1	180	2	D72629
82	67	5.1	183	2	A12274
83	67	5.1	213	2	A99104
84	67	5.1	231	2	S25738
85	66.5	5.1	153	2	S67294
86	66.5	5.1	197	2	B81720
87	66.5	5.1	216	2	T15317
88	66.5	5.1	228	2	T47425
89	66.5	5.1	232	2	S25756
90	66.5	5.1	234	2	S01320
91	66	5.1	119	2	B33876
92	66	5.1	135	2	JQ0472
93	66	5.1	167	2	S29579
94	66	5.1	192	2	E75541
95	66	5.1	195	2	B82443
96	66	5.1	226	2	T29210
97	66	5.1	228	2	S29575
98	66	5.1	235	2	S25759
99	65.5	5.0	181	2	T48558
100	65.5	5.0	188	2	S31952

translation elonga  
promastigote surfa  
mucin 3 (clone SIB  
Ig lambda chain V-  
pregnancy-specific  
UL4 protein - huma  
Ig lambda chain -  
pregnancy-specific  
Ras-like GTP-bindin  
hypothetical prote  
pregnancy-specific  
iduronate-2-sulfat  
probable enoyl-CoA  
Ig lambda chain -  
glial growth facto  
hypothetical prote  
probable acetyltra  
Ig lambda chain pr  
hypothetical prote  
cytolytic trigger  
hypothetical prote  
hypothetical prote  
T-cell surface gly  
Ig kappa chain V r  
recombination prot  
complement subcomp  
Ig lambda chain V  
ARWlambda protein  
alpha-amylose/subt  
Ig lambda chain -  
Ras-like GTP-bindin  
Ig heavy chain pre  
hypothetical prote  
hypothetical prote  
hypothetical prote  
OX-45 membrane gly  
hypothetical prote  
Ig gamma-1 chain -  
hypothetical prote  
probable chaperone  
T-cell receptor de  
pregnancy-specific  
hypothetical prote  
cytolytic trigger  
Ig heavy chain pre  
mucin 3 (clone SIB  
DNA-binding protei  
Ig light chain - s  
pregnancy-specific  
hypothetical prote  
hypothetical prote  
GTP-binding nuclea  
Ig lambda chain -  
hypothetical prote  
conserved hypothet  
hypothetical prote  
NAC domain-like pr  
Ig lambda chain -  
Ig kappa chain pre  
carcinoembryonic a  
T-cell receptor be  
Ig light chain - r  
MucT/nudix family  
Damx-related prote  
hypothetical prote  
Ig light chain - r  
Ig lambda chain -  
hypothetical prote  
penicillin-binding

ALIGNMENTS

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RESULT 1
G02630
FcalphaBb - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C;Accession: G02630
R;van Dijk, T.B.; Morton, H.C.; Caldenhoven, E.; Bracke, M.; Raaijmakers, J.A.M.; Lammer
submitted to the EMBL Data Library, April 1996
A;Reference number: H01508
A;Accession: G02630
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-239 <VAN>
A;Cross-references: UNIPROT:P24071; EMBL:U56236; NID:g1326228; PID:g1326229

Query Match      23.4%; Score 305; DB 2; Length 239;
Best Local Similarity 36.7%; Pred. No. 9.3e-17;
Matches 72; Conservative 34; Mismatches 78; Indels 12; Gaps 2;

Qy 1 QSGPLPKPSLQALPSSLVPLEKPYTLRCQPGVDLYRLEKLSRRYQD----- 49
Db 22 QEGDFMPFFISAKSPVILPGSVKIQCAIREAYLTQLMIKNSYIREIGRRLKFWNET 81

Qy 50 QAVLFIPAMKRSLAGRYCYSQNGSLWSLPDQLLELVATGVFAKPSLSAQPGPAVSSGGD 109
Db 82 DPEFVIDHMDANKAGRYCQYRIGHYFRYSDTLELVVTGLYKPFLSADRGVLMPGEN 141

Qy 110 VTLCQTRY-GFDQFALYKEGDPAPYKNPERWYASPIITVTAHSGTYRCYSFSSRDP 168
Db 142 ISLTCSAHPIPDFRSLAKEGELSLPQSGEHPANFSLGVDLNVSGIYRCYGYWNRSP 201

Qy 169 YLWSAPSDPLELVVTG 184
Db 202 YLWSFSPNALFLVVTG 217

RESULT 2
A42013
alpha-1-B-glycoprotein - North American opossum (fragments)
C;Species: Didelphis virginiana, Didelphis marsupialis virginiana (North American opossum)
C;Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 09-Jul-2004
C;Accession: A42013
R;Catanesse, J.J.; Kress, L.F.
Biochemistry 31, 410-418, 1992
A;Title: Isolation from opossum serum of a metalloproteinase inhibitor homologous to human
A;Reference number: A42013; MUID:92118834; PMID:1731898
A;Accession: A42013
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-237 <CAT>
A;Cross-references: UNIPROT:Q28359; GB:J05356
C;Keywords: glycoprotein

Query Match      11.1%; Score 145; DB 2; Length 237;
Best Local Similarity 29.4%; Pred. No. 0.00032;
Matches 58; Conservative 25; Mismatches 92; Indels 22; Gaps 10;

Qy 4 PLPKPSLQALPSSLVPLEKPYTLRCQGP-PGV--DLYR---LEKLSRRYQDQAVLETPA 57
Db 43 PLPAPSLRAEFGPWILRGVETKJHCRGVLGMIFDLYOEGEQEPVKSSHTTGTTEATFIV- 101

Qy 58 MKRSLAGRYCSYQ----NGSLWSLPDQLLELVATGVFAKPSLSAQPGPAVSSGGDVTLQ 113
Db 102 ---NSTGNYSLYRAPAPAPSVNSTPSETIHVILPDKANFYILNNRVRPRGDIYVS 158

Qy 114 CQTRYG---FD-QFALYKEGDPAPYK--NPERWYASPIITVTAHSGTYRC--YFSRR 166
Db 159 CQARFSEREYDLEFKLFDKQGETLVEVVLTSQMKVFDLTAVGPDGKGKYSCTRYFRNG 218

Qy 167 DPLWSAPSDPLELVVT 183
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Db 219 PP-INSSEDSNILELVVT 234

RESULT 3
T46433
hypothetical protein DKFZp434F0326.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accession: T46433
R;Ansorge, W.; Winkner, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000
A;Reference number: Z23028
A;Accession: T46433
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-184 <AAA>
A;Cross-references: UNIPROT:Q9NTC8; EMBL:AL137369
A;Experimental source: adult testis; clone DKFZp434F0326
C;Genetics:
A;Note: DKFZp434F0326.1

Query Match      10.9%; Score 141.5; DB 2; Length 184;
Best Local Similarity 38.8%; Pred. No. 0.00045;
Matches 38; Conservative 8; Mismatches 49; Indels 3; Gaps 1;

Qy 84 ELVATGVFAKPSLSAQPGPAVSSGGDVTLCQTRYGPDQFALYKEGDPAPYKNPERWYRA 143
Db 1 EIWVTDKPPKPSLSAWPSTMFKLKGKDIITLCQRLPGVEFLVLEHDSGEAPQQFSE---DG 57

Qy 144 SEPIITVTAHSGTYRCYSFSSRDPYLSAPSDDPLELV 181
Db 58 DFINNVEGKIGNYSYFLQAYPDIIWSEPSDPLELV 95

RESULT 4
G70512
probable lppK protein - Mycobacterium tuberculosis (strain H37Rv)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: G70512
R;Cole, S.T.; Broesch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.;
Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: G70512
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-189 <COL>
A;Cross-references: UNIPROT:O33251; GB:Z97559; GB:AL123456; NID:g3261820; PIDN:CAB10707.1
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: lppK

Query Match      6.8%; Score 88.5; DB 2; Length 189;
Best Local Similarity 25.1%; Pred. No. 6.6;
Matches 47; Conservative 24; Mismatches 81; Indels 35; Gaps 8;

Qy 68 CSYQNGSLWSLPDQLLELVATGVFAKPSLSAQPGPAVSSGGDVTLCQTRYGPDQFALYK 127
Db 23 CSHPEFKRSPFPAPSLPPVTSPPLEAAPIITLPAPEALI--DV-----LSR 66

Qy 128 EGPPA-PYKNPERWYRASFPFIIT-----VTAHSGTYRCYSFSSRDPYLS--APSDPL 178
Db 67 LADPAPGTVKNVQLLEGATPENAAALDRFTALRDSGLPMTFAAND-IASDNKPSDVM 125

Qy 179 ELVVTGTSVTPSRILPTPPSSVA-----EFSEATAELTVSFTNKVFTTERTSITTSPE 233
Db 126 ATVVVTTAHPDNREFTPFMEFVSFKGWQLSRQTAEMLLAMGNSPDSTPSA----TSPAP 181
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```
Qy 234 SDSPAGP 240
Db 182 APSPTPP 188

RESULT 5
S29577
Ig light chain - rainbow trout (fragment)
C:Species: Oncorhynchus mykiss (rainbow trout)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jul-2000
C:Accession: I51043; S29577
R: Dagdeldt, A.; Bengten, E.; Pilstrom, L.
Immunogenetics 38, 199-209, 1993
A:Title: A cluster type organization of the loci of the immunoglobulin light chain in A.
of cDNAs and hybridization analysis.
A:Reference number: I50732; MUID:93279739; PMID:8505063
A:Accession: I51043
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-233 <DA2>
A:Cross-references: EMBL:X68519; NID:G64175; PIDN:CAA48530.1; PID:G64176
C:Genetics: IGL
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin

Query Match 6.8%; Score 88.5; DB 2; Length 233;
Best Local Similarity 25.3%; Pred. No. 8.5;
Matches 41; Conservative 22; Mismatches 66; Indels 33; Gaps 7;

Qy 103 AVSSGGDVTLOCOT-----RY-----GPDQFALY-----KEGDAPYKNPE 138
Db 27 AVSGHVSLSCKTSSAVSDNGHYLHWYQKPGAPKLLIYWAKTLQSGTPSRFSGG 86

Qy 139 RWYRASPIITVTAHSGTYRCYFSSRDPLYWSAPSDPLELVVGTGTVTPSRLPTEPPS 198
Db 87 SGSDFTLISGQVADTDGYQCQSHSGPVVTFGSGT---RLDVGNSAPT-LTVLPSP 141

Qy 199 SVAEFSSEATLTVGFTNKKVFTTTS-----RSITTSPKESDSP 237
Db 142 S-EELSSTTTATLMCLANKGFPDWTIRKWDGTSQKQEASP 182

RESULT 6
S20000
Ig light chain precursor - rainbow trout
C:Species: Oncorhynchus mykiss (rainbow trout)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C:Accession: S20000; S29580
R: Dagdeldt, A.; Bengten, E.; Pilstrom, L.
submitted to the EMBL Data Library, March 1992
A:Reference number: S20000
A:Accession: S20000
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-235 <DAG>
A:Cross-references: EMBL:X65260; NID:G64181; PID:G64182
R: Dagdeldt, A.; Bengten, E.; Pilstrom, L.
submitted to the EMBL Data Library, September 1992
A:Description: A cluster type organisation of the loci of the immunoglobulin light chain
A:Reference number: S29569
A:Accession: S29580
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 122-133 <DA2>
A:Cross-references: EMBL:X68522; NID:G64180; PID:G938274
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:38-115/Domain: immunoglobulin homology <IMM>

Query Match 6.8%; Score 88.5; DB 2; Length 235;
Best Local Similarity 23.8%; Pred. No. 8.6;
Matches 57; Conservative 24; Mismatches 73; Indels 85; Gaps 13;
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```
Qy 24 VTLRCQ-----GPPGVDLVR-----LEKLSRRYQDQA-----VLFPI 55
Db 41 VTLRCFNKPPACSPPCVAVYQKPGAPQLLIYYATLQSGTFSRFGSGSGDFLITI 100

Qy 56 PAMKRSIAGRYRC-SYQNGSLWSLPS-DQLBLVATGVFAKPSLSAQP--GPAVSSGGDVT 111
Db 101 SGVQAEADAGDYQCQSHSGDVTWTFGSGTRLDV---GNSAPTLLTVLPSPSELSTTTAT 157

Qy 112 LQCOTRGVDFQFALYKSGDPAPYKPNRWYRASPFIITVTAHSGTYRCYFSSR----- 166
Db 158 LTCLANKGF-----PSDW-----TIRWKVDGPSQKQGTSSVLEKD 193

Qy 167 DPYLWSAPSDPLELVVGTGTVTPSRLPTEPPSPSVAEFSSEATLTVSTNKKVFTTETSR 225
Db 194 GLYSWSS-----TTLTIGLEWTKA-----GEVTCQAQNSQTS---VTKTLR 231

RESULT 7
PC4397
mucin 3 T10 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 10-Nov-1997 #sequence_revision 10-Nov-1997 #text_change 09-Jul-2004
C:Accession: PC4397
R: Van Klinken, B.J.W.; Van Dijken, T.C.; Oussoren, E.; Bueller, H.A.; Dekker, J.; Eimerha
Biochem. Biophys. Res. Commun. 238, 143-148, 1997
A:Title: Molecular cloning of human MUC3 cDNA reveals a novel 59 amino acid tandem repeat
A:Reference number: PC4395; MUID:97445141; PMID:9299468
A:Accession: PC4397
A:Molecule type: mRNA
A:Residues: 1-246 <VAN>
A:Cross-references: UNIPROT:O14762; DDBJ:AF016694; NID:G2454618; PIDN:AAB71687.1; PID:G24
A:Experimental source: intestine
F:1-46,47-105,106-164,165-223,224-246/Region: repeat

Query Match 6.8%; Score 88.5; DB 2; Length 246;
Best Local Similarity 25.3%; Pred. No. 9.1;
Matches 46; Conservative 19; Mismatches 68; Indels 49; Gaps 6;

Qy 69 SYQNGSLWSLPSDQLBLVATGVFAKPSLSAQP-GPAVSSGGDVTLOCOTRGVDFQFALYKE 128
Db 54 SSETSTLTTPADTSTPVTIYSQASSSPTTADGTSMT-----STVSE 96

Qy 129 GDPAPYKPNRWYRASPFIITVTAHSGTYRCYFSSRDPLYWSAPSDPLELVVGTGTVT 188
Db 97 GGTP-----LTSVPVSTTPV-----SSEASTLSTTPVDSPPVVTSTECT 137

Qy 189 PSRLPTEPPS-SVAEFSSEATAELT-----VSFTNKKVFTT--ETSRSITTSPKESD 235
Db 138 SSLTPTGCTSIATSPSGTPTPLTSMVPVTTTAVASSETNSLTTPADTTRTAVTTPVQASS 197

Qy 236 SP 237
Db 198 TP 199

RESULT 8
PC4396
mucin 3 T9 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 10-Nov-1997 #sequence_revision 10-Nov-1997 #text_change 09-Jul-2004
C:Accession: PC4396
R: Van Klinken, B.J.W.; Van Dijken, T.C.; Oussoren, E.; Bueller, H.A.; Dekker, J.; Eimerha
Biochem. Biophys. Res. Commun. 238, 143-148, 1997
A:Title: Molecular cloning of human MUC3 cDNA reveals a novel 59 amino acid tandem repeat
A:Reference number: PC4395; MUID:97445141; PMID:9299468
A:Accession: PC4396
A:Molecule type: mRNA
A:Residues: 1-236 <VAN>
A:Cross-references: UNIPROT:O14761; DDBJ:AF016693; NID:G2454616; PIDN:AAB71686.1; PID:G24
A:Experimental source: intestine
F:1-56,57-115,116-174,175-233,234-236/Region: repeat
```



C;Accession: G72548  
R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahara, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K DNA Res. 6, 83-101, 1999  
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum A;Reference number: A72450; MUID:99310339; PMID:10382966  
A;Accession: G72548  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-155 <Raw>  
A;Cross-references: UNIPROT:Q9YBC2; DDBJ:AP000062; NID:G5105244; PID:d1  
A;Experimental source: strain K1  
C;Genetics:  
A;Gene: APE1675

Query Match	6.1%	Score 79.5;	DB 2;	Length 155;
Best Local Similarity	23.1%	Pred. No. 26;		
Matches 43;	Conservative 18;	Mismatches 64;	Indels 61;	Gaps 8;

Qy		75	LWLSPSDQLLELVATGVFAKPSLSAQPGPAVSSGGDVTLQCQTRYGFDQFALYKEGDPPY	134
	:			
	:			
D <sub>b</sub>	11	LCWCP-----PLMPOOGLITRG-----TLYM----	PPL	36

[illegible]

QY 176 DPLELVVTCTSVTPSRLPTEPPSSVAEFSATAEL-TVSTFNKVTTTTSRSITTPSKES 234

QY
235 DSPAGP 240

RESULT 12  
AC3600  
cellulase (EC 3.2.1.4) [imported] - *Bruceella melitensis* (strain 16M)  
C/Species: *Bruceella melitensis*  
C/Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 09-Jul-2004  
C/Accession: AC3600  
R/DalVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,  
.; Mazur, M.; Gotsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letesee,  
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002  
A/Title: The genome sequence of the facultative intracellular pathogen *Bruceella melitensis*  
A/Reference number: AD3252; PMID:11756688  
A/Accession: AC3600  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-243 <KUR>  
A/Cross-references: UNIPROT:Q8YCL1; GB:AE008918; PIDN:AAL53966.1; PID:g17984913; GSPDB:G  
A/Experimental source: strain 16M  
C/Genetics:  
A/Gene: BMEI10724  
A/Map position: II  
C/Keywords: glycosidase; hydrolase

Query Match 6.1%; Score 79.5; DB 2; Length 243;  
Best Local Similarity 22.6%; Pred. No. 45;  
Matches 47; Conservative 23; Mismatches 61; Indels 77; Gaps 12;

QY	9	SLQALPSSLLVPLEKPVTLRCQ----	GGPG-VDLRYR-----	LEKLSSSR	46
ph	59	NMAVCSRAAKIKSPVTPHZAQEMEDDAGQFTWAEKPGGVYKAYRHHVIDYCRKSLPSAR			118

QY 47 YQDQAVLFIPAMKRSLAGRYCSCYQNGSLWSLPDQ-LELVATGVEAFKPSLSAQGPVAVS 105

Qy 106 SGGVTLQCOTRYGDFQFALYK-----EGD-----PAPYKNPERWYRASFPII 148

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Qy      149  TVTAAHSGTYRCYFSRSSDPYLWSAPSD 176
      |         |         |         |
Db      213  TAVV-----YFNDREVPW--PRD 229

RESULT 13
A21177
Ig light chain precursor V-J region - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 03-Aug-1990 #sequence_revision 03-Aug-1990 #text_change 21-Jan-2000
C:Accession: A21177; B22327
R:Reynaud, C.A.; Dahan, A.; Weill, J.C.
Proc. Natl. Acad. Sci. U.S.A. 80, 4099-4103, 1983
A:Title: Complete sequence of a chicken lambda light chain immunoglobulin derived from t
A:Reference number: A21177; MUID:83247424; PMID:6408641
A:Accession: A21177
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-213 <REY>
A:Cross-references: GB:K00678; NID:G212159; PIDN:AAA48906.1; PID:G212160
R:Reynaud, C.A.; Anquez, V.; Dahan, A.; Weill, J.C.
Cell 40, 283-291, 1985
A:Title: A single rearrangement event generates most of the chicken immunoglobulin light
A:Reference number: A90861; MUID:85099341; PMID:3917859
A:Accession: B22327
A:Molecule type: DNA
A:Residues: 98-110 <RE2>
A>Note: J region
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
P:20-92/Domain: immunoglobulin homology <IMW>

```

Query Match 6.1%; Score 79; DB 2; Length 213;  
Best Local Similarity 23.7%; Pred. No. 42;  
Matches 45: Conservative 19; Mismatches 82; Indels

QY	85	LVATGVFAKPSLSAQGPFAVS-----SGGDTVLCOTRYGFDQ-----FALYKEGDPA	133
nb	4	IIVCAAIITPASPASVANGPETVKIKTICSSGGCS-----YGWCOOKSPGSAPTVIYSNDKR	57

QY  
134 YKPNRW--YRASFPITVTAHSGTVRCYSFSRDPYLWSAPDPLELVVTGTSVT--188  
| | | | |  
50 CATHCECCCKSCSTMTITCVSEDEDAIVKECSVDY-----VGTECATTTTTL109

QY  
189 --PSRLPTPEP--PSSVAEPSEATAELTVSFTNKKVFTT-----ETGRSITTPKES 234

QY	235	DSPAGPARQY	244
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RESULT 14
JQ0473
T-cell receptor beta chain (BTb1) - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 30-May-1997
C:Accession: JQ0473
F:Tanaka, A.; Ishiguro, N.; Shinagawa, M.
submitted to JIPID, May 1990
A:Description: Sequence analysis of bovine T-cell receptor beta chain genes
A:Reference number: JQ0472

```

A;Accession: JQ0473  
A;Molecule type: mRNA  
A;Residues: 1-136 <TAN>  
A;Experimental source: T cell

C/Genetics:  
A/Gene: BTB1  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: T-cell receptor

```
Query Match          6.0%; Score 78.5; DB 2; Length 136;
Best Local Similarity 27.4%; Pred. No. 27; Mismatches 32; Indels 33; Gaps 7;
Matches 31; Conservative 17;

QY 92 AKPSLSAQPGAVSSGGDVTLOQQ-----TRYGFDQF-----ALYKE 128
DB 20 ALSSLS-PAAVSKSGASVIECRALDFQASSMFWYRQFPKRGVLWLMATNEGTDATEYEQ 78

QY 129 G--DPAFYKNPWRWYRASPIITVTAHSGTYRCYFSFSSRDPYLWMSAPSDPL 178
DB 79 GYNKDRFPISQDRTF--SSLWVISVDPTDSSLFYC---SARDSV--AADTQPL 125

RESULT 15
A40305
biliary glycoprotein - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 09-Jul-2004
C;Accession: A40305
R;Robbins, J.; Robbins, P.F.; Kozak, C.A.; Callahan, R.
Genomics 10, 583-587, 1991
A;Title: The mouse biliary glycoprotein gene (Bgp): partial nucleotide sequence, expressed
A;Reference number: A40305; MUID:91365364; PMID:1653760
A;Accession: A40305
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-206 <ROB>
A;Cross-references: UNIPROT:Q03679; GB:M61907; GB:M73534; NID:g192197; PIDN:AAA37298.1;
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-terminal
C;Keywords: Glycoprotein
F;2-51/Domain: immunoglobulin homology <IMM1>
F;87-144/Domain: immunoglobulin homology <IMM2>

Query Match          6.0%; Score 78; DB 2; Length 206;
Best Local Similarity 26.8%; Pred. No. 49;
Matches 33; Conservative 25; Mismatches 43; Indels 22; Gaps 6;

QY 4 PLPKPSLQALPSSVLPEKPVTLRC-OGPGVDLYRL-----EKLSSRYQDAVL 53
DB 71 PVTQPSLQVNTTVKELDS-VTLTCLSNIDIGANIQLWLFNSQSLQLTERMTLS--QNNIL 127

QY 54 FIPAMKSLAGRYRCSYQNG-SLWSPSDQLELV-----ATGVPAKPSLSAQPGPAV 104
DB 128 RIDPIKREDAGEYOCEISNPVSVKRSIKLIDIFDTQGLSDGATGIVIGAVAGVAL 187

QY 105 SSG 107
DB 188 IAG 190

RESULT 16
T40820
proline-rich protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T40820
R;Beck, A.; Reinhardt, R.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, October 1998
A;Reference number: Z21949
A;Accession: T40820
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-238 <BBC>
A;Cross-references: UNIPROT:O94274; EMBL:AL032684; PIDN:CAA21811.1; GSPDB:GN00067; SPDB:
A;Experimental source: strain 972h-; clone pl p887
C;Genetics:
A;Gene: SPDB:SPBP887.26
A;Map position: 2
C;Superfamily: proline-rich protein

Query Match          6.0%; Score 78; DB 2; Length 238;
Best Local Similarity 25.8%; Pred. No. 58;
Matches 46; Conservative 24; Mismatches 76; Indels 32; Gaps 9;
```

```
QY 74 SLWSPSDQLELVATGVFAKPSLS-----AOPG-----PAVSSGGDVTLOQTRYGFDQA 124
DB 51 STGSTPRTASPAVGNQDISKPSYSQSPSQPPKPEPALPSRGTPSL--PSRPGSRPSV 108

QY 125 LYKEGDPAPYKNPWRWYRASPIITVTAHSGTYRCYFSFSSRDPYLWMSAPSDPLELVVTG 184
DB 109 LNOEQVPPPPVPRPNVMSQMPPP--PSYSSSGSY-SQTYQSNANYTASSP-----LPTA 158

QY 185 TSVTPSRLLTEPPSPSSVAFSEATAELTVSFTHKVTFTTTSRSTTTSPKSSDSAPAGPAR 242
DB 159 SANAP--LPVPVPRRVSQNS-----SYASGVSPPAATAAS-TASFPVKKPPPPAPPK 205
```

```
RESULT 17
E75509
hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: E75509
R;White, O.; Eisen, J.A.; Heidelberg, J.P.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: E75509
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-138 <WHI>
A;Cross-references: UNIPROT:Q9RX00; GB:AE001910; GB:AE000513; NID:g6458198; PIDN:AAF1009;
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR0515
A;Map position: 1

Query Match          5.9%; Score 76.5; DB 2; Length 138;
Best Local Similarity 30.3%; Pred. No. 39;
Matches 23; Conservative 9; Mismatches 33; Indels 11; Gaps 2;

QY 168 PYLWSPSDPLELVVTGTSV--TPSRLPTEPPSSVAFSEATAELTVSFTHKVTFTTTSR 225
DB 58 PPLWAAMLDAALGLTAVPVEHTGTAQPVTPVSPQELDALTARITAA-----VRE 108

QY 226 SITTSPEKSDSPAGA 241
DB 109 ALGAAGSSTFSPAAPA 124
```

```
RESULT 18
JH0372
42K surface glycoprotein precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: JH0372; JH0373
R;Samman, W.E.; Niemi, E.C.; Stark, M.R.; Goldfien, R.D.; Pollock, A.S.; Imboden, J.B.
J. Exp. Med. 173, 251-260, 1991
A;Title: Molecular cloning of gp42, a cell-surface molecule that is selectively induced c
aling.
A;Reference number: JH0372; MUID:91086851; PMID:1845873
A;Accession: JH0372
A;Molecule type: mRNA
A;Residues: 1-233 <SEA>
A;Cross-references: UNIPROT:P33505; GB:X56448; NID:g56305; PIDN:CAA39831.1; PID:g56306
A;Experimental source: leukemia cell
A;Accession: JH0373
A;Molecule type: mRNA
A;Residues: 1-214, 'M', 216-233 <SE2>
C;Comment: This protein is induced on natural killer cells by interleukin 2.
C;Keywords: Glycoprotein
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-233/Product: 42K surface glycoprotein #status predicted <MAT>
F;29,66,181/Binding site: carbohydrate (Asn) (covalent) #status predicted
```



Query Match 5.9%; Score 76.5; DB 2; Length 233;  
Best Local Similarity 25.0%; Pred. No. 74;  
Matches 52; Conservative 34; Mismatches 71; Indels 51; Gaps 14;  
  
QY 8 PSLQALPSLVLEKPVTLRC-----QGPFGVDLVRLEKLSRRYQDQAVL-----53  
DB 23 PVLRLNSET---SDLLKCTTKVDNKPASELF-----YSFYKDNHIIQNRSHNPLF 73  
QY 54 FIPAMKRLAGRYC--SYQNGSLWSLSDLELVATGVFAKPSLSAQ--PGPAVSSGGDV 110  
DB 74 FISEANEENSGLYQCVDKADGTI--QKSDYLDIDLCTSVSQPVLTQLQHEATNLAEQDKV 132  
QY 111 TLQCTRYGF--DQFALYKED-----PAPYKNPERWTRASFPIITVTAHSG--TYRCYS 162  
DB 133 KFLCETQLGSLFYSFYMDGEILGELAPSG-----RAASLLISVKAESGKNYSQOA 186  
QY 163 PS--SRDPVLSAPSDP--LELVVTGTS 186  
DB 187 ENKVSRD-----ISEPKFPLVSGTA 208

## RESULT 19

S29594  
IG gamma chain (MM65) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 05-Nov-1999  
C:Accession: S29594  
R:Seymour, R.  
submitted to the EMBL Data Library, February 1991  
A:Reference number: S29593  
A:Accession: S29594  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-178 <SE>  
A:Cross-references: EMBL:X57857; NID:g52590; PIDN:CAA40992.1; PID:g52591  
C:Keywords: immunoglobulin

Query Match 5.8%; Score 75.5; DB 2; Length 178;  
Best Local Similarity 26.5%; Pred. No. 64;  
Matches 36; Conservative 16; Mismatches 63; Indels 21; Gaps 5;  
  
QY 83 LELVATGVFAKPSLSAQPGPAVSSGGDVTLCQTRYGDPQFALY-----KEG-----129  
DB 4 LMAVVTGVNSELVQLOQSGAELVKPGASVKLSC--TAGSNFKDVTYMHVVKQRPKQGLEWIG 62  
QY 130 --DPA--PYKNPERWTRASFPIITVTAHSGTYRCYSFSSRDPVLSAPSD-----PLELVV 182  
DB 63 RIDPANGTYEYDPKQGRATITADTSTNTAYLQLSLSTEDTAVYYCTGNGVAYGMDYWG 122  
QY 183 TGTSTVTPRLPTEPPS 198  
DB 123 QGTSVTSSAKTTPPS 138

## RESULT 20

I51920  
mucin - rhesus macaque (fragment)  
C:Species: Macaca mulatta (rhesus macaque)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C:Accession: I51920  
R:An, G.; Luo, G.; Wu, R.  
Am. J. Respir. Cell Mol. Biol. 10, 546-551, 1994  
A:Title: Expression of MUC2 gene is down-regulated by vitamin A at the transcriptional level  
A:Reference number: I51920; MUID:94235322; PMID:8179918  
A:Accession: I51920  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-216 <RES>  
A:Cross-references: UNIPROT:Q28501; EMBL:U00483; NID:g437054; PIDN:AAA20963.1; PID:g4370  
C:Genetics:  
A:Gene: MUC2

Query Match 5.8%; Score 75.5; DB 2; Length 216;  
Best Local Similarity 27.6%; Pred. No. 81;  
Matches 29; Conservative 15; Mismatches 40; Indels 21; Gaps 5;  
  
QY 144 SFPITVTAHSGTYRCYSFSSRDPVLSAPSDLELVVTGTSVTPSRLP--TEPPSSVA 201  
DB 75 STPIITTTTHTPT-----PTPTSTQTP--PTPIITTTTTPPTPTSTQTPPTTP 125  
QY 202 EFSATAELTVSFT-----NKVFTTTSRSITTSPEKSDSP 237  
DB 126 ITSNTTA-MTPTPTSTQTPVTPITTTTATPTPTPTSTQTP 169

## RESULT 21

JQ1263  
hypochemical 26K protein - foxtail mosaic virus  
C:Species: foxtail mosaic virus  
C:Date: 05-Mar-1993 #sequence\_revision 05-Mar-1993 #text\_change 18-Jun-1993  
C:Accession: JQ1263  
R:Bancroft, J.B.; Rouleau, M.; Johnston, R.; Prins, L.; Mackie, G.A.  
J. Gen. Virol. 72, 2173-2181, 1991  
A:Title: The entire nucleotide sequence of foxtail mosaic virus RNA.  
A:Reference number: JQ1258; MUID:91374015; PMID:1840610  
A:Accession: JQ1263  
A:Molecule type: genomic RNA  
A:Residues: 1-226 <BAN>  
A:Cross-references: GB:M62730

Query Match 5.8%; Score 75.5; DB 2; Length 226;  
Best Local Similarity 23.7%; Pred. No. 86;  
Matches 36; Conservative 19; Mismatches 44; Indels 53; Gaps 8;  
  
QY 14 PSSLVLEKPVTLRCQGP-----GVDLVRLEKLSRRYQDQAVLFIAPMKRSLAGRYCS 69  
DB 25 PSN-----ISKPRHCSGQPSRRGSOHLRRRTTQNSRPD---LWVTCFGSRTSGRW-CS 77  
QY 70 YONGSLWSLPSDQLVLVATGVFAKPSLSAQPGPAVSSGGDVTLCQTRYGDPQFALYK 129  
DB 78 QMS-----PSNLTQ-----SSGHHVQMRCK-----RPT 100  
QY 130 DPAPYKNPERWTRASFPIITVT-----AAHSG 156  
DB 101 SPSPYTRSRTEFFGNHPTLTGTNCRFSSSHSG 132

## RESULT 22

A56210  
neu differentiation factor - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 08-Sep-2002  
C:Accession: A56210  
R:Wen, D.; Suggs, S.V.; Karunakaran, D.; Liu, N.; Cupples, R.L.; Luo, Y.; Janseen, A.M.; Mol. Cell. Biol. 14, 1909-1919, 1994  
A:Title: Structural and functional aspects of the multiplicity of Neu differentiation factor  
A:Reference number: A56210; MUID:94158863; PMID:7509448  
A:Accession: A56210  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-230 <RES>  
A:Cross-references: EMBL:U02315; NID:g408380; PIDN:AAA19940.1; PID:g408381  
C:Superfamily: human heregulin; EGF homology; immunoglobulin homology

Query Match 5.8%; Score 75.5; DB 2; Length 230;  
Best Local Similarity 24.0%; Pred. No. 88;  
Matches 41; Conservative 21; Mismatches 80; Indels 29; Gaps 7;  
  
QY 89 GVEAKPS--LSAQPGPAV-----SSGGDVTLCQQT--RYGFDQFALYKEGDPA 133  
DB 8 GSRGKPGAEQDPSPALPRLKEMKQSQAAGSKLVLRCETSEYSSSLRFRKFKNGNELN 67  
QY 134 YQN-PE-----RWYRAFPIITVTAHSGTYRCYSFSSRDPVLSAPSDPLELVVTGTS 186  
DB 68 RKNKPENIKIQKKPGKSELINKASLADSGEYMWCKVSKLGN---DSASANTIVESNEF 124

Qy 187 VTPSRLPTE-----PPSSVAEFSSEATAELTVSFTHKVFTHETTSRSITTSKPKE 233  
Db 125 ITGMPASTETAYVSESPRISVTEGANTSSSTSTTGTHSLIKCAEKE 175

RESULT 23  
A86344  
protein T22111.8 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C:Accession: A86344  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719; PMID:11130712  
A:Accession: A86344  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-233 <STO>  
A:Cross-references: UNIPROT:Q9LPU4; GB:A8005172; NID:g8886992; PIDN:AAF80652.1; GSPDB:GN  
C:Genetics:  
A:Gene: T2211.8  
A:Map position: 1

Query Match 5.8%; Score 75.5; DB 2; Length 233;  
Best Local Similarity 21.9%; Pred. No. 89;  
Matches 39; Conservative 27; Mismatches 45; Indels 67; Gaps 11;

Qy 90 VFAPSLSAQ-----PCPAVSSGGDVTLCQCTRYGDFQFALYKEGD----- 130  
Db 22 LFSPSLSATFLVDGVSVKWSPTVHTGDSV8---KHKYGIDLY-IFRNKDAFVNCFTQA 77

Qy 131 ---PAPYKNPERWYRASFPITITAAHSGTYRCYFSFSRDPYLSAP-----SDPLELVV 182  
Db 78 TLLTKPNSSTFWY-----PSRTGSY-YFSFTNNT---SLPKTCQLNQLTVQV 122

Qy 183 TGTSVTPSRLTEPSPSSVAEFSSEATAELTVSFTHKVFTHETTSRSITTSKPESDSPAG 240  
Db 123 ILAAASP---PSQPP-----ATAPVPV8-----EGGVISPPSSYPWPLGP 159

RESULT 24  
PC2022  
mucin like protein Muc2 precursor - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 14-Jul-1994 #sequence\_revision 14-Jul-1994 #text\_change 16-Aug-2004  
C:Accession: PC2022  
R:Hansson, G.C.; Baekstroem, D.; Carlstedt, I.; Klinga-Levan, K.  
Biochem. Biophys. Res. Commun. 198, 181-190, 1994  
A:Title: Molecular cloning of a cDNA coding for a region of an apoprotein from the 'inco  
A:Reference number: PC2022; MUID:94121629; PMID:8292021  
A:Accession: PC2022  
A:Molecule type: mRNA  
A:Residues: 1-235 <HAN>  
A:Cross-references: UNIPROT:Q63349; GB:Z29072; NID:g435534; PIDN:CAA82313.1; PID:g435535  
C:Experimental source: intestine  
C:Genetics:  
A:Gene: muc2  
A:Map position: 1  
C:Superfamily: von Willebrand factor type A repeat homology; von Willebrand factor type  
C:Keywords: glycoprotein  
F:1-53/Region: cysteine-rich  
F:54-235/Region: serine/threonine-rich

Query Match 5.8%; Score 75; DB 2; Length 235;

Best Local Similarity 27.5%; Pred. No. 98;  
Matches 33; Conservative 15; Mismatches 48; Indels 24; Gaps 6;

Qy 135 KNPERWYRASFPITITVTAHSGTYRCYFSFSRDPYLSAPSDPLELVVTVTGTSTVTPSRLPT 194  
Db 25 KNAEQGIGGIIPMRMCLNVEINVCCICITS-----TPPSTTTEIQTT-TSTTKTSIPT 77

Qy 195 -----PPSSVAEFSSEATA---ELTVSFTHKVFTHETTSRSITTSKPESDSPA 238  
Db 78 STAMKTPSPSFTTTPPTPTTTTQISTSTSTTKITPTTETSTPSTT-SQTPSPA 136

RESULT 25  
S25755  
Ig lambda chain - human  
C:Species: Homo sapiens (man)  
C:Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C:Accession: S25755  
R:Combratio, G.; Klobbeck, H.G.  
Eur. J. Immunol. 21, 1513-1522, 1991  
A:Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam  
A:Reference number: S16439; MUID:91257162; PMID:1904362  
A:Accession: S25755  
A:Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-243 <COM>  
A:Cross-references: EMBL:X57820; NID:g33739; PIDN:CAA40957.1; PID:g33740  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:158-226/Domain: immunoglobulin homology <IMM>

Query Match 5.8%; Score 75; DB 2; Length 243;  
Best Local Similarity 23.9%; Pred. No. 1e+02;  
Matches 48; Conservative 25; Mismatches 98; Indels 30; Gaps 8;

Qy 76 WSLPSDQLELVATGCVFAKPSLSAQPGPAVSSGGDVTLCQCTRYGFD-----QFALYKEG 129  
Db 3 WTLTLLVLLSHCTGSLSQPVLTQPSHSHSAGSASVRLTCLSSGFSVGDFWIRWYQKPG 62

Qy 130 DPAPY-----KNPERWYRASFPITITVTAHSGTYRCYFSFS---SRDPY---LNSAPS 175  
Db 63 NPPRYLLYHSDSNKGGQSGVPSRFGSGNSDASANAGILRISGLQLEVEADYYCGTWHSNS 122

Qy 176 DPLELVVTVTGTSTVTPSRLTEPSPSSVAEFSSEATAELTVSFTHKVFTHETTSRSITTSKPKE 233  
Db 123 KNKRVFGGFGTKLVLGQPKAAP-SVTLPSPSSELOANKATLVCLISDFYFGAVTVAWKA 181

Qy 234 SDSP--AG-----PARQYYTK 247  
Db 182 DSSPVKAGVETTTTPSKQSNK 202

Search completed: October 29, 2005, 03:47:39  
Job time : 44 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 29, 2005, 03:36:42 ; Search time 172 Seconds  
(without alignments)  
741.324 Million cell updates/sec

Title: US-09-503-387-3\_COPY\_21\_269

Perfect score: 1304

Sequence: 1 QSGPLPRLPSLQALPSSLVPL.....SPKESDSPAGPARQYTKGN 249

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 824343

Minimum DB seq length: 0

Maximum DB seq length: 250

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : UniProt 03:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	321	24.6	244	2	Q8MI78	Q8mi78 pongo pygma
2	314.5	24.1	193	2	Q6PI73	Q6pi73 homo sapien
3	312.5	24.0	239	2	Q9UPI8	Q9upi8 homo sapien
4	301.5	23.1	203	2	Q9UNC4	Q9unc4 homo sapien
5	296.5	22.7	202	2	Q00382	Q00382 homo sapien
6	292.5	22.4	202	2	Q00380	Q00380 homo sapien
7	291.5	22.4	221	2	Q9UQL7	Q9uql7 homo sapien
8	291	22.3	220	2	Q8N741	Q8n741 homo sapien
9	288.5	22.1	203	2	Q9UNB9	Q9unb9 homo sapien
10	288.5	22.1	203	2	Q9UNC6	Q9unc6 homo sapien
11	287.5	22.0	203	2	Q9UNC0	Q9unc0 homo sapien
12	287.5	22.0	203	2	Q9UNC5	Q9unc5 homo sapien
13	282.5	21.7	202	2	Q00381	Q00381 homo sapien
14	282.5	21.7	203	2	Q9UNC2	Q9unc2 homo sapien
15	279.5	21.4	170	2	Q9UNC7	Q9unc7 homo sapien
16	278.5	21.4	203	2	Q9UNC1	Q9unc1 homo sapien
17	278.5	21.4	203	2	Q9UNC7	Q9unc7 homo sapien
18	276.5	21.2	246	2	Q8M738	Q8m738 macaca mula
19	269.5	20.7	203	2	Q9UNC3	Q9unc3 homo sapien
20	259.5	19.9	236	2	Q6QWD6	Q6qwd6 homo sapien
21	255.5	19.6	235	2	Q6QWD5	Q6qwd5 homo sapien
22	247.5	19.0	235	2	Q6QWD4	Q6qwd4 homo sapien
23	245	18.8	174	2	Q8MI79	Q8mi79 pongo pygma
24	244.5	18.8	227	2	Q9H7L2	Q9h7l2 homo sapien
25	238	18.3	151	2	Q95702	Q95702 homo sapien
26	238	18.3	163	2	Q9UQA2	Q9uqa2 homo sapien
27	225	17.3	204	2	Q14950	Q14950 homo sapien
28	224	17.2	247	2	Q8N736	Q8n736 homo sapien
29	223.5	17.1	240	2	Q8MK01	Q8mk01 macaca mula
30	217	16.6	245	2	Q00547	Q00547 homo sapien
31	213.5	16.4	209	2	Q92588	Q92588 homo sapien

32	213.5	16.4	212	2	Q95L80	Q95l80 macaca mula
33	212.5	16.3	157	2	Q8MK14	Q8mk14 macaca mula
34	210.5	16.1	164	2	Q43394	Q43394 homo sapien
35	210.5	16.1	230	2	Q8N738	Q8n738 homo sapien
36	210.5	16.1	241	2	Q8MK22	Q8mk22 macaca mula
37	210	16.1	178	2	Q8MJ29	Q8mj29 macaca mula
38	207.5	15.9	247	2	Q8MK24	Q8mk24 macaca mula
39	202.5	15.5	242	2	Q8N6C5	Q8n6c5 homo sapien
40	200.5	15.4	223	2	Q6R4Z5	Q6r4z5 ovib aries
41	200.5	15.4	232	2	Q8NHJ0	Q8nhj0 homo sapien
42	199	15.3	222	2	Q86VI6	Q86vi6 homo sapien
43	197.5	15.1	169	2	Q8MK13	Q8mk13 macaca mula
44	195.5	15.0	239	2	Q6H2G6	Q6h2g6 homo sapien
45	193.5	14.8	119	2	Q8MK00	Q8mk00 macaca mula
46	193.5	14.8	233	2	Q925N5	Q925n5 rattus norv
47	193	14.8	125	2	Q78200	Q78200 homo sapien
48	193	14.8	186	2	Q95L79	Q95l79 macaca mula
49	191.5	14.7	153	2	Q9UNB5	Q9unb5 homo sapien
50	191.5	14.7	178	2	Q92592	Q92592 homo sapien
51	190.5	14.6	232	2	Q8BMN5	Q8bmns mus musculu
52	189.5	14.5	161	2	Q95L78	Q95l78 macaca mula
53	188.5	14.5	243	2	Q92803	Q92803 homo sapien
54	188	14.4	206	2	Q14949	Q14949 homo sapien
55	183.5	14.1	229	2	Q8MK21	Q8mk21 macaca mula
56	170.5	13.1	152	2	Q6ISS4	Q6iss4 homo sapien
57	163	12.5	166	2	Q9UNB4	Q9unb4 homo sapien
58	162.5	12.5	105	2	Q9UNB6	Q9unb6 homo sapien
59	160.5	12.3	138	2	Q6QWD7	Q6qwd7 homo sapien
60	160	12.3	152	2	Q6QWD9	Q6qwd9 homo sapien
61	150.5	11.5	105	2	Q9UNB8	Q9unb8 homo sapien
62	147	11.3	143	2	Q86VI5	Q86vi5 homo sapien
63	145	11.1	211	2	Q28359	Q28359 didelphis m
64	144.5	11.1	130	2	Q96L49	Q96l49 homo sapien
65	144.5	11.0	144	2	Q96L47	Q96l47 homo sapien
66	143.5	11.0	109	2	Q96L48	Q96l48 homo sapien
67	142.5	10.9	95	2	Q8NHJ5	Q8nhj5 homo sapien
68	141.5	10.9	184	2	Q9NUTC8	Q9ntc8 homo sapien
69	135	10.4	236	2	Q6UX27	Q6ux27 homo sapien
70	126.5	9.7	225	2	Q96PJ1	Q96pj1 homo sapien
71	125.5	9.6	219	2	Q96PJ4	Q96pj4 homo sapien
72	122.5	9.4	248	2	Q9JKL2	Q9jkl2 rattus norv
73	121	9.3	208	2	Q8C233	Q8c233 mus musculu
74	109.5	8.4	179	2	Q92587	Q92587 homo sapien
75	109.5	8.4	205	2	Q92591	Q92591 homo sapien
76	109.5	8.4	217	2	Q92589	Q92589 homo sapien
77	98	7.5	226	2	Q8N440	Q8n440 homo sapien
78	94	7.2	235	2	Q6PIK1	Q6pik1 homo sapien
79	93	7.1	63	2	Q6PEZ4	Q6pez4 homo sapien
80	93	7.1	230	2	Q8C6N8	Q8c6n8 mus musculu
81	92	7.1	64	2	Q75755	Q75755 homo sapien
82	92	7.1	247	2	Q9MUL5	Q9mul5 mus musculu
83	91.5	7.0	236	2	Q90696	Q90696 bovine herp
84	91.5	7.0	243	2	Q39501	Q39501 bovine herp
85	91.5	7.0	248	2	Q9D074	Q9d074 mus musculu
86	89	6.8	171	2	Q95N20	Q95n20 sus scrofa
87	88.5	6.8	189	1	LPK_MYCTU	LPK_MYCTU mycobacteri
88	88.5	6.8	189	1	LPK_MYCTU	LPK_MYCTU mycobacteri
89	88.5	6.8	246	2	Q14762	Q14762 homo sapien
90	87	6.7	236	2	Q14761	Q14761 homo sapien
91	86.5	6.6	250	2	Q7SEF8	Q7sef8 neurospora
92	86	6.6	233	1	FC3B_HUMAN	FC3B_HUMAN
93	86	6.6	249	2	Q82LM6	Q82lm6 streptomyce
94	86	6.6	250	1	FCG3_BOVIN	FCG3_BOVIN
95	85.5	6.6	114	2	Q8H2N0	Q8h2n0 oryza sativ
96	85.5	6.6	127	2	Q9QMB1	Q9qmb1 human immun
97	85.5	6.6	154	2	Q8N733	Q8n733 homo sapien
98	85.5	6.6	224	2	Q7T5F2	Q7t5f2 cercopithe
99	85.5	6.6	243	2	Q806C8	Q806c8 cercopithe
100	82.5	6.3	148	2	Q84167	Q84167 chlamydia t

ALIGNMENTS

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RESULT 1
ID Q8MI78 PRELIMINARY; PRT; 244 AA.
AC Q8MI78;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Natural killer cell immunoglobulin-like receptor (Fragment).
GN Name=Popy-KIR2DL4;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22072192; PubMed=12077248;
RA Guethlein L.A., Flodin L.R., Adams E.J., Parham P.;
RT "NK cell receptors of the orangutan (Pongo pygmaeus): a pivotal
RT species for cracking the coevolution of killer cell Ig-like receptors
RT with MHC-C.";
RL EMBL; AF470389; AAM78489.1; -.
DR HSP; P43628; I86U.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR KW Receptor.
FT NON TER.
SQ SEQUENCE 1 1
244 AA; 27269 MW; BF67E2177E659FB6 CRC64;

Query Match 24.6%; Score 321; DB 2; Length 244;
Best Local Similarity 36.2%; Pred. No. 3.8e-17;
Matches 84; Conservative 34; Mismatches 92; Indels 22; Gaps 7;

Qy 7 KPSLQALPSSLVPLEKPYTLRCQPPGVLDYLRLEKLS-----SRVQDAVLFIAMK 59
Db 1 KPFCASWPSAVVPGGHVTLRCHYRRGNFIPTLYKDGVPPELYNRFMNSPLISP-VT 59
Qy 60 RSLAGRYRC---SYONGSLWSPDLQELVATGFAKPSLSAQPGPAVSSGGDVTLOCOT 116
Db 60 PAHAGTRCRGPHSPTEWAPSPLVIVMTGTYEKPSLSAQPGPTVRAGENVTLSGSS 119
Qy 117 RYGDQFALYKEDPAPYKNP-----ERWYRASPIITVTAAHSGTYRCYSFSSRDPLYW 171
Db 120 WSSFDWYHLSREGEAQLRLPAVPSINGTFOADFFL--GPATHRGTYRCFGSPRGSPV 177
Qy 172 SAPSDPLELVGTGTSVTPSRLPTEP--PSSVAEFSAEATLTVFTWNVFTT 221
Db 178 SDPSDPLLVSTGTPSSSWPSTPSTFGIARHLHAVIRYSAII--LEFTT 227

RESULT 2
ID Q6PI73 PRELIMINARY; PRT; 193 AA.
AC Q6PI73;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE LIURB2 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL EMBL; BC041708; AAH41708.1; -.
DR HSP; P43628; I86U.
DR InterPro; IPR007110; IG-like.
DR SEQUENCE 193 AA; 21175 MW; 6721E1740AC1BDDA CRC64;

Query Match 24.1%; Score 314.5; DB 2; Length 193;
Best Local Similarity 41.4%; Pred. No. 9.1e-17;
Matches 70; Conservative 28; Mismatches 56; Indels 15; Gaps 3;

Qy 1 QSGPLPKPSLQALPSSLVPLEKPYTLRCQPPGVLDYLRLEKLSRRYQD-----QA 51
Db 22 QAGFPFKPTLWAEPPGVSIVTWCQGLSRAQEQYLDKGEPSPELDNRNPLEPKKA 81
Qy 52 VLPIPMKRSLAGRYRCYONGSLWSPDLQELVATGFAKPSLSAQPGPAVSSGGDVT 111
Db 82 RFSIPSTQTHAGRYRCHYSSAGNSEPSDPLELVMTGTYKFTLSALPFPVVASGGM 141
Qy 112 LQCTRYGDFQFALYKED---PAPYKNP---RWYRASPIITVTAAH 154
Db 142 LRCSQKGYHHFVLMKEGHEQLPRTLDSQQLHSGGFOALFPVGPVTPSH 190

RESULT 3
ID Q9UPI8 PRELIMINARY; PRT; 239 AA.
AC Q9UPI8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Natural killer associated transcript 2 (Fragment).
GN Name=KIR2DL3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,
RA Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,
RA Phan H., Velasco N., Do L., Regala W., Terry A., Ganes J.,
RA Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,
RA Attix C., Andreise T., Frankheim M., Amico-Keller G., Coefield J.,
RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,
RA Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
RA Olsen A.S., Carrano A.V.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC006293; AAD03160.1; -.
DR HSP; P43628; I86U.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG; 2.
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DR SMART; SM00409; IG; 1.
FT NON TER 239
SQ SEQUENCE 239 AA; 26113 MW; 9AD66A23B4A8F35E CRC64;

Query Match 24.0%; Score 312.5; DB 2; Length 239;
Best Local Similarity 37.4%; Pred. No. 1.7e-16;
Matches 82; Conservative 24; Mismatches 76; Indels 37; Gaps 7;

QY 7 KPSLOALPSSLVPLEKPVTLRCQGGPPGVDLYRLEKLSRSSRYQD-----QAVL 53
DB 28 KPSLLAHPGLVKSEETVILQWSDVRQHFLLHR--EGKFKDTLHLIGEHDGSKANF 85

QY 54 FIPAMKRSIAGRYRC-----SYQNGSLWSLPDQLELVATGVFAKPSLSAQPGPVS 106
DB 86 SIGPMWQDLAGTYRCYGVSVTHSPYQ----LSAPSDPLDIVITGLYEKPSLSAQPGPTVLA 141

QY 107 GGDVTLQCTRYGFDQFALYKEGD-----PAPYKNERWYRASFPFIITVTAHSGTYR 159
DB 142 GESVTLSCSSRSSYDMYHLSREGEAHERRFAGPKVNGT--FQADFPL--GPATHGGTYR 197

QY 160 CYFSRRDPYLSAPSDPLELVVTGTSVTPSRLPTEPSS 198
DB 198 CFGSPRDSFYEWNSSDPLLVSVTGNPSNFWPSPTEPSS 236

RESULT 4
QYUNCA4 PRELIMINARY; PRT; 203 AA.
ID QYUNCA4;
AC QYUNCA4;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE P58 killer cell inhibitory receptor KIR-K36 (Fragment).
GN Name=KIR-K36;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99351717; PubMed=10424431; DOI=10.1016/S0165-2478(99)00062-0;
RA Chwaee Y.J., Cho S.E., Kim S.J., Kim J.;
RT "Diversity of the repertoire of p58 killer cell inhibitory receptors
in a single individual.";
RL Immunol. Lett. 68:267-274(1999).
DR EMBL; U96190; AAB54120.1; -.
DR HSSP; P43628; 1B6U.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 1.
KW Receptor.
FT NON TER 1
SQ SEQUENCE 203 AA; 22347 MW; D256BB1EEF4AF122 CRC64;

Query Match 23.1%; Score 301.5; DB 2; Length 203;
Best Local Similarity 38.7%; Pred. No. 1e-15;
Matches 79; Conservative 26; Mismatches 64; Indels 35; Gaps 8;

QY 7 KPSLOALPSSLVPLEKPVTLRCQGGPPGVDLYRLEKLSRSSRYQD-----QAVL 53
DB 7 KPSLLAHPGLVKSEETVILQWSDVRQHFLLHR--EGKFKDTLHLIGEHDGSKANF 64

QY 54 FIPAMKRSIAGRYRC-----SYQNGSLWSLPDQLELVATGVFAKPSLSAQPGPVS 106
DB 65 SIGPMWQDLAGTYRCYGVSVTHSPYQ----LSAPSDPLDIVITGLYEKPSLSAQPGPTVLA 120

QY 107 GGDVTLQCTRYGFDQFALYKEGD-----ERYRASFPFIITVTAHSGTYR 161

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DB 121 GENVTLCSSRSSYDMYHLSREGEAHERRLPAVRSSINGTQADFPL--GPATHGGTYRCP 178
QY 162 SFSSRD-PYLWSAPSDPLELVVTG 184
DB 179 G-SFRDAPYEWNSSDPLLVSVTG 201

RESULT 5
O00382 PRELIMINARY; PRT; 202 AA.
ID O00382;
AC O00382;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE P58 NK cell inhibitory receptor NKR-K7 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99351717; PubMed=10424431; DOI=10.1016/S0165-2478(99)00062-0;
RA Chwaee Y.J., Cho S.E., Kim S.J., Kim J.;
RT "Diversity of the repertoire of p58 killer cell inhibitory receptors
in a single individual.";
RL Immunol. Lett. 68:267-274(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98018248; PubMed=9378975;
RA Kim J., Chwaee Y.J., Kim S.J., Choi I.H., Park J.H., Kim S.J.;
RT "Molecular basis of HLA-C recognition by p58 natural killer cell
inhibitory receptors.";
RL J. Immunol. 159:3875-3882(1997).
DR EMBL; U96190; AAB54120.1; -.
DR HSSP; P43628; 1B6U.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 1.
KW Receptor.
FT NON TER 1
SQ SEQUENCE 202 AA; 22182 MW; C15D7330639FF82B CRC64;

Query Match 22.7%; Score 296.5; DB 2; Length 202;
Best Local Similarity 37.6%; Pred. No. 2.4e-15;
Matches 77; Conservative 24; Mismatches 67; Indels 37; Gaps 7;

QY 7 KPSLOALPSSLVPLEKPVTLRCQGGPPGVDLYRLEKLSRSSRYQD-----QAVL 53
DB 7 KPSLLAHPGLVKSEETVILQWSDVRQHFLLHR--EGKFKDTLHLIGEHDGSKANF 64

QY 54 FIPAMKRSIAGRYRC-----SYQNGSLWSLPDQLELVATGVFAKPSLSAQPGPVS 106
DB 65 SIGPMWQDLAGTYRCYGVSVTHSPYQ----LSAPSDPLDIVITGLYEKPSLSAQPGPTVLA 120

QY 107 GGDVTLQCTRYGFDQFALYKEGD-----PAPYKNERWYRASFPFIITVTAHSGTYR 159
DB 121 GESVTLSCSSRSSYDMYHLSREGEAHERRFAGPKVNGT--FQADFPL--GPATHGGTYR 176

QY 160 CYFSRRDPYLSAPSDPLELVVTG 184
DB 177 CFGSPRDSFYEWNSSDPLLVSVTG 201

RESULT 6
O00380 PRELIMINARY; PRT; 202 AA.
ID O00380;
AC O00380;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

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Db 145 SCSSQSSFDIYHLSREGEAHELRLPAVPSINGTQADFFL--GPATHTCYRCGSPHGS 202
Qy 168 PYLWSAPSDPLELVVTG 184
Db 203 PYEWSDPDPLFVSVTG 219

RESULT 9
Q9UNB9 PRELIMINARY; PRT; 203 AA.
AC Q9UNB9;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE P58 killer cell inhibitory receptor KIR-K78 (Fragment).
GN Name=KIR-K78;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99351717; PubMed=10424431; DOI=10.1016/S0165-2478(99)00062-0;
RA Chwaee Y.J., Cho S.E., Kim S.J., Kim J.;
RT "Diversity of the repertoire of p58 killer cell inhibitory receptors
in a single individual.";
RL Immunol. Lett. 68:267-274(1999).
DR HSP; P43626; INKR.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 203
SQ SEQUENCE 203 AA; 22299 MW; E5D5CCC37B3EE102 CRC64;

Query Match 22.1%; Score 288.5; DB 2; Length 203;
Best Local Similarity 37.6%; Pred. No. 1e-14;
Matches 77; Conservative 22; Mismatches 69; Indels 37; Gaps 7;

Qy 7 KPSLOALPSSLVPLEKPVTLRCQPPGVYLRLEKLSRRYQD-----QAVL 53
Db 7 KPSLLAHPRGLVKSEETVILQCWSDVMEFHFLLHR--EGMFNDTLRLIGEHHGVSKANF 64
Qy 54 FIPAKESLAGRYRC-----SYONGSLWLSPLSDQLVATGVFAKPSLSAQPGPAVSS 106
Db 65 SISRTQDLAGTYRCYGSVTHSPYQ-----VSAPSDPLDIVITGCEKPSLSAQPGPTVLA 120
Qy 107 GGVTLQCQTRYGDFQALYKEGD-----PAPYKNPERWYRASFFIITVTAHSGTYR 159
Db 121 GESVTLSCSSRSSYDMYHLSREGEAHERRFSAGPKVNGT--FQADFFL--GPATHTGGTYR 176
Qy 160 CYSFSSRDPLYWSAPSDPLELVVTG 184
Db 177 GSFHSDPYEWSKSDPLLVSVTG 201

RESULT 11
Q9UNCO PRELIMINARY; PRT; 203 AA.
AC Q9UNCO;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE P58 killer cell inhibitory receptor KIR-K65 (Fragment).
GN Name=KIR-K65;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99351717; PubMed=10424431; DOI=10.1016/S0165-2478(99)00062-0;
RA Chwaee Y.J., Cho S.E., Kim S.J., Kim J.;
RT "Diversity of the repertoire of p58 killer cell inhibitory receptors
in a single individual.";
RL Immunol. Lett. 68:267-274(1999).
DR HSP; P43628; 1B6U.
DR GO; GO:0005887; C:integral to plasma membrane; NAS.
DR GO; GO:0030110; F:HLA-C specific inhibitory MHC class I recep. . .; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR GO; GO:0030102; P:negative regulation of natural killer cell . . .; NAS.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 203
SQ SEQUENCE 203 AA; 22256 MW; 91FFF6C166B0C4A8 CRC64;

Query Match 22.1%; Score 288.5; DB 2; Length 203;
Best Local Similarity 37.9%; Pred. No. 1e-14;
Matches 77; Conservative 24; Mismatches 69; Indels 33; Gaps 7;

Qy 7 KPSLOALPSSLVPLEKPVTLRCQPPGVY---LYRLEKLSRRY-----QDQAVLFI 55
Db 7 KPSFLALPGHLVKSEETVILQCWSDVMEFHFLLHREGKFNNTLHIGEHHDGVSKANFSI 66
Qy 56 PAKESLAGRYRC-----SYONGSLWLSPLSDQLVATGVFAKPSLSAQPGPAVSSGG 108
Db 67 GPMMPVLAGTYRCYGSVTHSPYQ-----LSAPSDPLDMVIIIGLYEKPSSLSAQPGPTVLAGE 122
Qy 109 DVTLCQTRYGDFQALYKEGD-----PAPYKNPERWYRASFFIITVTAHSGTYRCY 161
Db 123 SVTLSCSSRSSYDMYHLSREGEAHERRFSAGPKVNGT--FQADFFL--GPATHTGGTYRCF 178
Qy 162 SFSSRDPLYWSAPSDPLELVVTG 184
Db 179 GSFHSDPYEWSKSDPLLVSVTG 201

RESULT 10
Q9UNC6 PRELIMINARY; PRT; 203 AA.
AC Q9UNC6;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE P58 killer cell inhibitory receptor KIR-K9 (Fragment).
GN Name=KIR-K9;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99351717; PubMed=10424431; DOI=10.1016/S0165-2478(99)00062-0;
RA Chwaee Y.J., Cho S.E., Kim S.J., Kim J.;
RT "Diversity of the repertoire of p58 killer cell inhibitory receptors
in a single individual.";
RL Immunol. Lett. 68:267-274(1999).
DR EMBL; AF135555; AAD48763.1; -.
DR HSP; P43626; INKR.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 203
SQ SEQUENCE 203 AA; 22299 MW; E5D5CCC37B3EE102 CRC64;

Query Match 22.1%; Score 288.5; DB 2; Length 203;
Best Local Similarity 37.6%; Pred. No. 1e-14;
Matches 77; Conservative 22; Mismatches 69; Indels 37; Gaps 7;

Qy 7 KPSLOALPSSLVPLEKPVTLRCQPPGVYLRLEKLSRRYQD-----QAVL 53
Db 7 KPSLLAHPRGLVKSEETVILQCWSDVMEFHFLLHR--EGMFNDTLRLIGEHHGVSKANF 64
Qy 54 FIPAKESLAGRYRC-----SYONGSLWLSPLSDQLVATGVFAKPSLSAQPGPAVSS 106
Db 65 SISRTQDLAGTYRCYGSVTHSPYQ-----VSAPSDPLDIVITGCEKPSLSAQPGPTVLA 120
Qy 107 GGVTLQCQTRYGDFQALYKEGD-----PAPYKNPERWYRASFFIITVTAHSGTYR 159
Db 121 GESVTLSCSSRSSYDMYHLSREGEAHERRFSAGPKVNGT--FQADFFL--GPATHTGGTYR 176
Qy 160 CYSFSSRDPLYWSAPSDPLELVVTG 184
Db 177 CFSFRSDPYEWSKSDPLLVSVTG 201

RESULT 11
Q9UNCO PRELIMINARY; PRT; 203 AA.
AC Q9UNCO;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE P58 killer cell inhibitory receptor KIR-K65 (Fragment).
GN Name=KIR-K65;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99351717; PubMed=10424431; DOI=10.1016/S0165-2478(99)00062-0;
RA Chwaee Y.J., Cho S.E., Kim S.J., Kim J.;
RT "Diversity of the repertoire of p58 killer cell inhibitory receptors
in a single individual.";
RL Immunol. Lett. 68:267-274(1999).
DR EMBL; AF135561; AAD48769.1; -.
DR HSP; P43628; 1B6U.
DR GO; GO:0005887; C:integral to plasma membrane; NAS.
DR GO; GO:0030110; F:HLA-C specific inhibitory MHC class I recep. . .; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR GO; GO:0030102; P:negative regulation of natural killer cell . . .; NAS.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 203
SQ SEQUENCE 203 AA; 22299 MW; E5D5CCC37B3EE102 CRC64;

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SQ SEQUENCE 203 AA; 22235 MW; 224B332DC781D01A CRC64;
Query Match 22.0%; Score 287.5; DB 2; Length 203;
Best Local Similarity 37.8%; Pred. No. 1.2e-14;
Matches 76; Conservative 26; Mismatches 70; Indels 29; Gaps 6;

QY 7 KPSLQALPSSLVPLEKPVTLRCQPPGVD---LYRLEKLSRRY-----QDAVLFI 55
DB 7 KPSFLAHPGHLVVKSEETVILQCWSVDMVFEHLLHREGKFNNTLHLIGEHDGVSKANFSI 66
QY 56 PAMKRSLAGRYRC-----SYQNGSLWSLPSDQELVATGVFAKPSLSAQPGPAVSSG 108
DB 67 GPMMPVLAGTYRCYGVSHSPYQ-----LSAPSDPLDIVITGLYKPSLSAQLGPTVLA 122
QY 109 DVTLCQOTRYGFDQFALYKEGDPAPYKNP-----ERWYRASFPITVTAHSGTYRCY 163
DB 123 NVTLSCSSRSYDMVHLSREGEAHERRLPAGPKVNGTFOADPFL--GPATHGTYRCFGS 180
QY 164 SSRDPYLWSAPSDPLELVVTG 184
DB 181 FHDSPYEWSSSDPLLVSVTG 201

RESULT 12
ID Q9UNC5 PRELIMINARY; PRT; 203 AA.
AC Q9UNC5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE P58 killer cell inhibitory receptor KIR-K15 (Fragment).
GN Name=KIR-K15;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1];
RP SEQUENCE FROM N.A.
RA Chwae Y.J., Cho S.E., Kim S.J., Kim J.;
RT "Diversity of the repertoire of p58 killer cell inhibitory receptors
in a single individual.";
RL Immunol. Lett. 68:267-274 (1999).
DR EMBL; AF135556; AAD48764.1; -.
DR HSP; P43627; 1EFX.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; IG.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 1.
DR KIR Receptor.
FT NON TER
FT NON TER
SQ SEQUENCE 203 AA; 22350 MW; 76A2E919BE8AF2FA CRC64;
Query Match 22.0%; Score 287.5; DB 2; Length 203;
Best Local Similarity 38.2%; Pred. No. 1.2e-14;
Matches 78; Conservative 24; Mismatches 67; Indels 35; Gaps 8;

QY 7 KPSLQALPSSLVPLEKPVTLRCQPPGVDLYRLEKLSRRYQD-----QAVL 53
DB 7 KPSLLAHPGRVLVKSEETVILQCWSVDMVFEHLLHREGKFNNTLHLIGEHDGVSKANF 64
QY 54 FIPAMKRSLAGRYRC-----SYQNGSLWSLPSDQELVATGVFAKPSLSAQPGPAVSS 106
DB 65 SIGPMMPVLAGTYRCYGVSHSPYQ-----LSAPSDPLDMVITGLYKPSLSAQPGPTVQA 120
QY 107 GGDVTLQOTRYGFDQFALYKEGDPAPYKNP-----ERWYRASFPITVTAHSGTYRCY 161
DB 121 GENVTLSRSSYDMVHLSREGEAHERRLPAVRKNGTFOADPFL--GPATHGTYRCF 178
QY 162 SFSSRD-PYLWSAPSDPLELVVTG 184
DB 179 GSFHDSPEYWSKSDPLLVSVTG 201

RESULT 14
ID Q9UNC2 PRELIMINARY; PRT; 203 AA.
AC Q9UNC2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE P58 killer cell inhibitory receptor KIR-K61 (Fragment).
GN Name=KIR-K61;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1];
RP SEQUENCE FROM N.A.
RA Kim J., Chwae Y.J., Kim M.Y., Choi I.H., Park J.H., Kim S.J.;
RT "Molecular basis of HLA-C recognition by p58 natural killer cell
inhibitory receptors.";
RL J. Immunol. 159:3875-3882 (1997).
DR EMBL; U96189; AAB54119.1; -.
DR HSP; P43626; INKR.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 1.
DR KIR Receptor.
FT NON TER
FT NON TER
SQ SEQUENCE 202 AA; 22282 MW; 71F892D914202069 CRC64;
Query Match 21.7%; Score 282.5; DB 2; Length 202;
Best Local Similarity 36.5%; Pred. No. 3e-14;
Matches 74; Conservative 25; Mismatches 71; Indels 33; Gaps 6;

QY 7 KPSLQALPSSLVPLEKPVTLRCQPPGVDLYRLEKLSRRYQD-----QAVL 53
DB 7 KPSLLAHPGRVLVKSEETVILQCWSVDMVFEHLLHREGKFNNTLHLIGEHDGVSKANF 64
QY 54 FIPAMKRSLAGRYRC-----SYQNGSLWSLPSDQELVATGVFAKPSLSAQPGPAVSS 106
DB 65 SISRMTPDLAGTYRCYGVSHSPYQ-----VSAPSDPLDIVITGLYKPSLSAQLGPTVLA 120
QY 107 GGDVTLQOTRYGFDQFALYKEGDPAPYKNP-----ERWYRASFPITVTAHSGTYRCY 161
DB 121 GENVTLSRSSYDMVHLSREGEAHERRLPAGPKVNGTFOADPFL--GPATHGTYRCF 178
QY 162 SFSSRD-PYLWSAPSDPLELVVTG 184
DB 179 GSFHDSPEYWSKSDPLLVSVTG 201
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Db 179 G-SFRDAPYEWSSSDPLLVSVTG 201

RESULT 13
ID O00381 PRELIMINARY; PRT; 202 AA.
AC O00381;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE P58 NK cell inhibitory receptor NKR-K6 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1];
RP SEQUENCE FROM N.A.
RA Chwae Y.J., Cho S.E., Kim S.J., Kim J.;
RT "Diversity of the repertoire of p58 killer cell inhibitory receptors
in a single individual.";
RL Immunol. Lett. 68:267-274 (1999).
DR EMBL; U96189; AAB54119.1; -.
DR HSP; P43626; INKR.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 1.
DR KIR Receptor.
FT NON TER
FT NON TER
SQ SEQUENCE 202 AA; 22282 MW; 71F892D914202069 CRC64;
Query Match 21.7%; Score 282.5; DB 2; Length 202;
Best Local Similarity 36.5%; Pred. No. 3e-14;
Matches 74; Conservative 25; Mismatches 71; Indels 33; Gaps 6;

QY 7 KPSLQALPSSLVPLEKPVTLRCQPPGVDLYRLEKLSRRYQD-----QAVL 53
DB 7 KPSLLAHPGRVLVKSEETVILQCWSVDMVFEHLLHREGKFNNTLHLIGEHDGVSKANF 64
QY 54 FIPAMKRSLAGRYRC-----SYQNGSLWSLPSDQELVATGVFAKPSLSAQPGPAVSS 106
DB 65 SISRMTPDLAGTYRCYGVSHSPYQ-----VSAPSDPLDIVITGLYKPSLSAQLGPTVLA 120
QY 107 GGDVTLQOTRYGFDQFALYKEGDPAPYKNP-----ERWYRASFPITVTAHSGTYRCY 161
DB 121 GENVTLSRSSYDMVHLSREGEAHERRLPAGPKVNGTFOADPFL--GPATHGTYRCF 178
QY 162 SFSSRD-PYLWSAPSDPLELVVTG 184
DB 179 GSFHDSPEYWSKSDPLLVSVTG 201

RESULT 14
ID Q9UNC2 PRELIMINARY; PRT; 203 AA.
AC Q9UNC2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE P58 killer cell inhibitory receptor KIR-K61 (Fragment).
GN Name=KIR-K61;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1];
RP SEQUENCE FROM N.A.
RA Kim J., Chwae Y.J., Kim M.Y., Choi I.H., Park J.H., Kim S.J.;
RT "Molecular basis of HLA-C recognition by p58 natural killer cell
inhibitory receptors.";
RL J. Immunol. 159:3875-3882 (1997).
DR EMBL; U96189; AAB54119.1; -.
DR HSP; P43626; INKR.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 1.
DR KIR Receptor.
FT NON TER
FT NON TER
SQ SEQUENCE 202 AA; 22282 MW; 71F892D914202069 CRC64;
Query Match 21.7%; Score 282.5; DB 2; Length 202;
Best Local Similarity 36.5%; Pred. No. 3e-14;
Matches 74; Conservative 25; Mismatches 71; Indels 33; Gaps 6;

QY 7 KPSLQALPSSLVPLEKPVTLRCQPPGVDLYRLEKLSRRYQD-----QAVL 53
DB 7 KPSLLAHPGRVLVKSEETVILQCWSVDMVFEHLLHREGKFNNTLHLIGEHDGVSKANF 64
QY 54 FIPAMKRSLAGRYRC-----SYQNGSLWSLPSDQELVATGVFAKPSLSAQPGPAVSS 106
DB 65 SISRMTPDLAGTYRCYGVSHSPYQ-----VSAPSDPLDIVITGLYKPSLSAQLGPTVLA 120
QY 107 GGDVTLQOTRYGFDQFALYKEGDPAPYKNP-----ERWYRASFPITVTAHSGTYRCY 161
DB 121 GENVTLSRSSYDMVHLSREGEAHERRLPAGPKVNGTFOADPFL--GPATHGTYRCF 178
QY 162 SFSSRD-PYLWSAPSDPLELVVTG 184
DB 179 GSFHDSPEYWSKSDPLLVSVTG 201
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OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99351717; PubMed=10424431; DOI=10.1016/S0165-2478(99)00062-0;
RA Chwaee Y.J., Cho S.E., Kim S.J., Kim J.;
RT "Diversity of the repertoire of p58 killer cell inhibitory receptors
in a single individual.";
RL Immunol. Lett. 68:267-274(1999).
DR EMBL; AF135559; AAD48767.1; -.
DR HSSP; P43626; INKR.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; IG.
DR DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 1.
DR KW Receptor.
FT NON_TER 1
FT NON_TER 203
SQ SEQUENCE 203 AA; 22275 MW; BD27C0F96AC03FAD CRC64;

Query Match 21.7%; Score 282.5; DB 2; Length 203;
Best Local Similarity 37.3%; Pred. No. 3e-14;
Matches 75; Conservative 26; Mismatches 71; Indels 29; Gaps 6;

QY 7 KPSLOALPSSILVPLEKPVTLRCQPGVD--LVREKLSSRY-----QQAVALFI 55
DB 7 KPSFLALPGHLVKSEETVILQCSVDVMEFHLHREGKFNTHLHIGEHGVSKANFSI 66
QY 56 PAMKRSLAGRYRC-----SYQNGSLWSPDQLELVATGVFAKPSLSAQPGPAVSSGG 108
DB 67 GPMVPVLATGYCYGSPVHPYQ-----LSAFSDPLDMVIIIGLYEKPSLSAQGLPTVLAGE 122
QY 109 DVTLCQTRYGDFQALYKEGDPAPYKNP-----ERWYRASFPITVTAAHSGTYRCYSF 163
DB 123 NVTLSCSSRSYDMYHLSREGEAHERRLPAVRSGTNGTQADFPFL--GPATHGGTYRCFGS 180
QY 164 SSRDPYLSAPSDPLELVVTG 184
DB 181 FHDSPIYEWKSDPLLVSVTG 201

RESULT 15
QYUNB7 PRELIMINARY; PRT; 170 AA.
AC Q9UNB7
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE P50 killer cell activating receptor KAR-K1d (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99351717; PubMed=10424431; DOI=10.1016/S0165-2478(99)00062-0;
RA Chwaee Y.J., Cho S.E., Kim S.J., Kim J.;
RT "Diversity of the repertoire of p58 killer cell inhibitory receptors
in a single individual.";
RL Immunol. Lett. 68:267-274(1999).
DR EMBL; AF135564; AAD48758.1; -.
DR HSSP; P43626; INKR.
DR GO; GO:0005887; C:integral to plasma membrane; NAS.
DR GO; GO:0030110; F:HLA-C specific inhibitory MHC class I recep. . .; NAS.
DR GO; GO:006955; P:immune response; NAS.
DR GO; GO:003102; P:negative regulation of natural killer cell . . .; NAS.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00409; IG; 1.
DR KW Receptor.
FT NON_TER 1
FT NON_TER 170
SQ SEQUENCE 170 AA; 18819 MW; 1174C8AEB0115FEA CRC64;
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Query Match 21.4%; Score 279.5; DB 2; Length 170;
Best Local Similarity 37.7%; Pred. No. 4.2e-14;
Matches 72; Conservative 22; Mismatches 56; Indels 41; Gaps 7;

QY 7 KPSLOALPSSILVPLEKPVTLRCQPGVDLVRLKLSRSSRYQDQAVLFIPAMKRSLAGRY 66
DB 7 KPSFLALPGHLVKSEETVILQCSVDVMEFHLHREGKFNTHLHIGEHGVSKANFSI 45
QY 67 RC-----SYQNGSLWSPDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLCQTRYG 119
DB 46 RCYGSVPHSPYQ-----LSAFSDPLDMVIIIGLYEKPSLSAQPGPTVQAGENVTLSCSSRS 101
QY 120 FDFQALYKEGDPAPYKNP-----ERWYRASFPITVTAAHSGTYRCYSFSSRD--PYLWSA 173
DB 102 YDMYHLSREGEAHERRLPAVRSGTNGTQADFPFL--GPATHGGTYRCFG--SPRDAPYEMSN 158
QY 174 PSDPLELVVTG 184
DB 159 SSDPLLVSVTG 169

RESULT 16
QYUNCI PRELIMINARY; PRT; 203 AA.
AC Q9UNCI
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE P58 killer cell inhibitory receptor KIR-K64 (Fragment).
GN Name=KIR-K64;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99351717; PubMed=10424431; DOI=10.1016/S0165-2478(99)00062-0;
RA Chwaee Y.J., Cho S.E., Kim S.J., Kim J.;
RT "Diversity of the repertoire of p58 killer cell inhibitory receptors
in a single individual.";
RL Immunol. Lett. 68:267-274(1999).
DR EMBL; AF135560; AAD48768.1; -.
DR HSSP; P43626; INKR.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 1.
DR KW Receptor.
FT NON_TER 1
FT NON_TER 203
SQ SEQUENCE 203 AA; 22474 MW; 1486649A1BF15ED65 CRC64;

Query Match 21.4%; Score 278.5; DB 2; Length 203;
Best Local Similarity 36.0%; Pred. No. 6.2e-14;
Matches 73; Conservative 25; Mismatches 72; Indels 33; Gaps 6;

QY 7 KPSLOALPSSILVPLEKPVTLRCQPGVDLVRLKLSRSSRYD-----QAVL 53
DB 7 KPSFLALPGHLVKSEETVILQCSVDVMEFHLHREGKFNTHLHIGEHGVSKANF 64
QY 54 FIPAMKRSLAGRYRC-----SYQNGSLWSPDQLELVATGVFAKPSLSAQPGPAVSS 106
DB 65 SISRTQDLAGTYRCYGVTHSPYQ-----VSAPSDPLDIVIIGLYEKPSLSAQGLPTVLA 120
QY 107 GGDVTLCQTRYGDFQALYKEGDPAPYKNP-----ERWYRASFPITVTAAHSGTYRCY 161
DB 121 GENVTILSCSSRSYDMYHLSREGEAHERRLPAVRSGTNGTQADFPFL--GPATHGGTYRCF 178
QY 162 SFSSRDPLYWSAPSDPLELVVTG 184
DB 179 GSFHDSPIYEWKSDPLLVSVTG 201
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RA Hershberger K.L., Shyam R., Miura A., Letvin N.L.;
RT "Diversity of the killer cell Ig-like receptors of rhesus monkeys.";
RL J. Immunol. 166:4380-4390 (2001).
DR EMBL; AF334658; AAK26819.1; -.
DR HSP; P24071; IOVZ.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 1.
KW Receptor.
FT NON_TER
SQ SEQUENCE 246 AA; 27374 MW; 4DA9B93AE874C15B CRC64;

Query Match 21.4%; Score 276.5; DB 2; Length 246;
Best Local Similarity 36.1%; Pred. No. 1.1e-13;
Matches 78; Conservative 32; Mismatches 75; Indels 31; Gaps 8;

QY 2 SGPLPKPSLQALPSSLVPLEKPVTLRCQPPGV-----DLYRLEK----LSSSRVQDOA 51
DB 17 TGGQDKIFLSVQPSALVPQGGHMTLRCHYRRGLYNTFNFTLYKDDRHSHVFIHNRIFQES 76
QY 52 VLFIPAMKRLSLAGRYRC--SYQNG-SLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGG 108
DB 77 FLMGVTPPAD-AGTYRCRGSYPHSPTEWSALSDFLAIMVTGVHRKPSLLALPGPLVKSGE 135
QY 109 DVTLCQOTRYGDFQFALYKEGDPAPYKNPERWY-----RASFPITVTAHSGTYRC 160
DB 136 TVTLQCSSDTVFHFHFLHSE--VNFEPKPLHLVGELHGGGSOANYSINSKTSDLAETYRC 192
QY 161 YSFSSRDPPYLWSAPSDPLELVVTGTSVTPSRLPTEP 196
DB 193 YGSVTHSPYVLSAPSDPLDIVTG-----RLPSPG 222

RESULT 19
Q9UNC3 PRELIMINARY; PRT; 203 AA.
AC Q9UNC3;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE P58 killer cell inhibitory receptor KIR-K39 (Fragment).
DN Name=KIR-K39;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99351717; PubMed=10424431; DOI=10.1016/S0165-2478(99)00062-0;
RA Chwaee Y.J., Cho S.E., Kim S.J., Kim J.;
RT "Diversity of the repertoire of p58 killer cell inhibitory receptors
in a single individual.";
RL Immunol. Lett. 68:267-274 (1999).
DR HSP; P43626; INKR.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 1.
KW Receptor.
FT NON_TER
SQ SEQUENCE 203 AA; 22414 MW; 9BFD4CC138A779CA CRC64;

Query Match 21.4%; Score 278.5; DB 2; Length 203;
Best Local Similarity 36.6%; Pred. No. 6.2e-14;
Matches 75; Conservative 24; Mismatches 69; Indels 37; Gaps 7;

QY 7 KPSLQALPSSLVPLEKPVTLRCQPPGVLDLYRLEKLSRRYQD-----QAVL 53
DB 7 KPSLLAHPLGRLVKSEETVILQCWSDFVMEHFLHRL--EGMENDTLRLIGEHHDGVSXANF 64
QY 54 FIPAMKRLSLAGRYRC-----SYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSS 106
DB 65 SISRTQDLAGTYRCYGSVTHSPYQ-----VSAPSDPLDIVIIGLYEKPSLSAQGLPTVLA 120
QY 107 GGDVTLQOTRYGDFQFALYKEGD-----PAPYKNPERWYRASFPITVTAHSGTYR 159
DB 121 GENTLSCSSSSYDMYHLSREGAHERFRFSAGPKVNGT--FQADFFL--GPATHGGTYR 176
QY 160 CYFSFSSRDPPYLWSAPSDPLELVVTG 184
DB 177 CFGSFRDSPYEWNSSDPLLVSVTG 201

RESULT 18
Q8MJZ8 PRELIMINARY; PRT; 246 AA.
AC Q8MJZ8;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Killer immunoglobulin-like receptor KIR3DH splice variant 7 (Fragment).
DN Name=KIR3DH;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21154036; PubMed=11254692;

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QY 7 KPSLQALPSSLYPLEKPVTLRCQPPGVLDLRLKLSRRYQDQAV-----LFI 55  
DB 7 KPSLLAHPGLKSGETVILQCSWDVMEHFHFLHRDISEDPSRLVGQIHGVSXANFSI 66  
QY 56 PAMKRSAGRYRC-----SYQNGSLWSPDQLELVATGVFAKPSLSAQPGPAVSSGG 108  
DB 67 GPLMPVLAGTRCYGVSVPYQ-----LSAFSDPLDIVITGLYKPSLSAQGLPTVLAGE 122  
QY 109 DVTLOQCTRYGDFDQALYKEGDPAPYKNP-----ERWTRASFPIITVTAHSGTYRCYSF 163  
DB 123 NVTLSCSSRSSYDMVHLSREGEAHERRLPAGPKVNGTFOADFPPL--GPATHGGTYRCFGS 180  
QY 164 SSRDPYLWSPDPLELVVTG 184  
DB 181 FHDSPIYEWKSSDPLLVSVTG 201

## RESULT 20

Q6QWD6 PRELIMINARY; PRT; 236 AA.  
AC Q6QWD6;  
DT 05-JUL-2004 (TRENBLrel. 27, Created)  
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)  
DE 05-JUL-2004 (TRENBLrel. 27, Last annotation update)  
DE KIR antigen 3DL1 (Fragment).  
GN Name=KIR3DL1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP Schammel C.M.G., Hurley C.K.;  
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY523804; AAS73160.1; JOINED.  
DR EMBL; AY523805; AAS73160.1; JOINED.  
DR EMBL; AY523806; AAS73160.1; --  
DR HSSP; P43628; 1B6U.  
DR InterPro; IPR007110; Ig-like.  
DR Pfam; PF00047; ig; 2.  
FT NON\_TER 1  
FT NON\_TER 236  
SQ SEQUENCE 236 AA; 25828 MW; 9959A3DD2378CF81 CRC64;

Query Match 19.9%; Score 259.5; DB 2; Length 236;  
Best Local Similarity 37.1%; Pred. No. 2.3e-12;  
Matches 69; Conservative 20; Mismatches 68; Indels 29; Gaps 5;

QY 7 KPSLQALPSSLYPLEKPVTLRCQPPGVLDLRLKLSRRYQDQAV-----LFI 55  
DB 57 KPSLLAHPGLKSGERVILQCSWDIMPFHFLHKEGISKDPSRLVGQIHGVSXANFSI 116  
QY 56 PAMKRSAGRYRC-----SYQNGSLWSPDQLELVATGVFAKPSLSAQPGPAVSSGG 108  
DB 117 GPMLALAGTRCYGVSVTHSQ-----LSAPSDPLDIVITGPKPSLSAQPGPKVQAGE 172  
QY 109 DVTLOQCTRYGDFDQALYKEGDPAPYKNP-----ERWTRASFPIITVTAHSGTYRCYSF 163  
DB 173 SVTLSCSSRSSYDMVHLSREGEAHERRLPAVRKVNRTFOADFPPL--GPATHGGTYRCFGS 230  
QY 164 SSRDPY 169  
DB 231 FRHSPY 236

## RESULT 21

Q6QWD5 PRELIMINARY; PRT; 235 AA.  
AC Q6QWD5;  
DT 05-JUL-2004 (TRENBLrel. 27, Created)  
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)  
DE KIR antigen 3DL2 (Fragment).

GN Name=KIR3DL2;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP Schammel C.M.G., Hurley C.K.;  
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY523807; AAS73161.1; JOINED.  
DR EMBL; AY523808; AAS73161.1; JOINED.  
DR EMBL; AY523809; AAS73161.1; --  
DR HSSP; P43628; 1B6U.  
DR InterPro; IPR007110; Ig-like.  
DR Pfam; PF00047; ig; 2.  
FT NON\_TER 1  
FT NON\_TER 235  
SQ SEQUENCE 235 AA; 25771 MW; F56803C029B09258 CRC64;

Query Match 19.6%; Score 255.5; DB 2; Length 235;  
Best Local Similarity 34.5%; Pred. No. 4.7e-12;  
Matches 70; Conservative 26; Mismatches 76; Indels 31; Gaps 7;

QY 63 AGRYRCYQNGSL-----WSLPDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLOQOT 116  
DB 24 AGTYRC---RGSRPHSLSLTGWSPTSNPLVIMVTGNHRKPSLLAHPGLKSGETVILQCS 80  
QY 117 RYGDQFALYKEGDPAPYKNP---RASEPFIITVTAHSGTYRCYSFSSRDP 168  
DB 81 DVMFEHFFLHREGIS---EDPSRLVGQIHGVSXANFSIGLMPVLGTYRCYGVSPHP 137  
QY 169 YLWSPDPLELVVTGTSVTPSRLPTEPPSSVAEFSAEITVSTFKVFTTET----- 223  
DB 138 YQLSAPSDPLDIVITGLYKPS-LSAQPGTVQAGENVTLSCSSWSYDIYHLSREGEAH 196  
QY 224 SRSITTSKP-----ESDSPAGPA 241  
DB 197 ERLRAVPKVNRTFOADFPGLPA 219

## RESULT 22

Q6QWD4 PRELIMINARY; PRT; 235 AA.  
AC Q6QWD4;  
DT 05-JUL-2004 (TRENBLrel. 27, Created)  
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)  
DE KIR antigen 3DL2 (Fragment).  
GN Name=KIR3DL2;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP Schammel C.M.G., Hurley C.K.;  
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY523810; AAS73162.1; JOINED.  
DR EMBL; AY523811; AAS73162.1; JOINED.  
DR EMBL; AY523812; AAS73162.1; --  
DR HSSP; P43628; 1B6U.  
DR InterPro; IPR007110; Ig-like.  
DR Pfam; PF00047; ig; 2.  
FT NON\_TER 1  
FT NON\_TER 235  
SQ SEQUENCE 235 AA; 25745 MW; 8E0A8100E839AB2D CRC64;

Query Match 19.0%; Score 247.5; DB 2; Length 235;  
Best Local Similarity 34.0%; Pred. No. 2e-11;  
Matches 69; Conservative 26; Mismatches 77; Indels 31; Gaps 7;

QY 63 AGRYRCYQNGSL-----WSLPDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLOQOT 116  
DB 24 AGTYRC---RGSRPHSLSLTGWSPTSNPLVIMVTGNHRKPSLLAHPGLKSGETVILQCS 80

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Db 24 AGTYRC---RGRSHSLTGWSPAPNPLVIMVGNHRRKPSLLAHPTGLKSGTIVLQWS 80
Qy 117 RYGDQFALYKEGDPAPYKQPERWY-----RASPIITVTAAHSGTTRCYFSFSRDP 168
Db 81 DVMEHFHFLREGIS---EDPSRLVGQIHDCGSKANFSIGPLMEVLVLAGTTRCYGVSVPSP 137
Qy 169 YLWSAPSDPLELVVTGTSVTPSRPLTPPPSSVAFSEATAELTVSFINKVPTTET----- 223
Db 138 YQSAPSDPLEDITVIGLYERKS--LSAQPGPTVQAGENVTLSCSSWSSDIYHLSRREGAH 196
Qy 224 SRSITTSFK-----ESDSPAGPA 241
Db 197 ERRLRVAPKVNRTQADFLGPA 219

RESULT 23
Q8MI79 ID Q8MI79 PRELIMINARY; PRT; 174 AA.
AC Q8MI79,
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Natural killer cell immunoglobulin-like receptor (Fragment).
GN Name=Popv-KIR2DL4;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22072192; PubMed=12077248;
RA Guethlein L.A., Flodin L.R., Adams E.J., Parham P.;
RT "NK cell receptors of the orangutan (Pongo pygmaeus): a pivotal
RT species for tracking the coevolution of killer cell Ig-like receptors
RT with MHC-C.";
RL J. Immunol. 169:220-229(2002).
DR EMBL; AF470388; AA078488.1; -.
DR HSP; P43626; INKR.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 1.
KW Receptor.
FT NON TER 1
FT SEQUENCE 174 AA; 19227 MW; F3C5FDC8FC316C39 CRC64;

Query Match 18.8%; Score 245; DB 2; Length 174;
Best Local Similarity 36.5%; Pred. No. 2.1e-11;
Matches 62; Conservative 27; Mismatches 63; Indels 18; Gaps 5;

Qy 7 KPSLQALPSSLVPLEKPVTLRCQGGPPGVDLYRLEKLS-----SRVQDQAVLFIAMK 59
Db 1 KPFCASNPASVAVPQGGHVLTRCHYRRGNIFTLKDGVPVPELYNRIFWNSPLISP-VT 59
Qy 60 RSLAGRTRC-----SYQNSLWLSPLSDQLELVATGVFAKPSLSAQPGPAVSSGDVTLQCT 116
Db 60 PAHAGTYRCRGFHPSPSTWSPAPNPLVIMVGTGYERKPSLSAQPGPTVCAGENVTLSCSS 119
Qy 117 RYGDQFALYKEGDPAPYKQNP-----ERWYRASFPITVTAAHSGTTRCY 161
Db 120 WSSFDVHLSREGEAHQLRLPAVPSINGTFQADFLP--GPATHRGTTRCP 167

RESULT 24
Q9H7L2 ID Q9H7L2 PRELIMINARY; PRT; 227 AA.
AC Q9H7L2,
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE FLJ00060 protein (Fragment).
GN Name=FLJ00060;

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Spleen; DOI=10.1038/ngi1285;
RX PubMed=14702039;
RA Oca T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahara K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamiyama K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Ninomiya K., Ihibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hiroaka S., Chiba Y., Ishida S.,
RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshihara K., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Inagaki H., Ikema Y., Okamoto S.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Itoh T., Shigeta K., Senba T.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Morinaga M., Sasaki M.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Komatsu T.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs";
RT Nat. Genet. 36:40-45(2004).
RL EMBL; AK024467; BAB15757.1; -.
DR HSP; P43627; 2DLI.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; ig; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 1
FT SEQUENCE 227 AA; 25153 MW; FD0D56B81F5D0F75 CRC64;

Query Match 18.8%; Score 244.5; DB 2; Length 227;
Best Local Similarity 31.1%; Pred. No. 3.2e-11;
Matches 71; Conservative 26; Mismatches 74; Indels 57; Gaps 7;

Qy 2 SGLPKPSLQALPSSLVPLEKPVTLRCQGGPGVD---LYRLEKLSRRYQDQ----- 50
Db 7 SGLTKPSISAGHPSLHVAGARVSLRCHSELAFDEFTLYKEGHIQHSQQLDQGMAGIHY 66
Qy 51 --AVLFPAMKRSLSAGYRC-----SYQNSLWLSPLSDQLELVATGVFAKPSLSAQPG 101
Db 67 VEAVFSGMPTPAHAGAYRCGCFSHRYE-----WSAPSDPLDITVITGKPKSLSTQVD 122
Qy 102 PAVSSGGDVTLCQCTRYGDFQFALYKEGDPAPYKQNP-----YRASFPITVT 151
Db 123 PMRLGKGLTLCSSSEISFDQYHLFRHG-----VAHQWLSSGGQRHREAFQANFSVGRAT 177
Qy 152 AAHSGTTRCYFSFSRDPY-----LWSAPSDPLELV 181
Db 178 PVPGETRYCYGFSFNDSPYKPPVTRCNFTPQETLRVLLCHSQNPPLNLV 225

RESULT 25
Q99702 ID Q99702 PRELIMINARY; PRT; 151 AA.
AC Q99702,
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
```

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DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)
DE 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
OS Putative inhibitory receptor (fragment).
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97131668; PubMed=8977169;
RA Rojo S., Burshtyn D.N., Long E.O., Wagtmann N.;
RT "Type I transmembrane receptor with inhibitory function in mouse mast
cells and NK cells.";
RL J. Immunol. 158:9-12(1997).
DR EMBL; U70665; AAC50928.1; -.
DR HSP; Q8NHL6; IGX.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Receptor.
FT NON_TER 151 151
SQ SEQUENCE 151 AA; 16464 MW; CE589A6D278C2C1B CRC64;

Query Match 18.3%; Score 238; DB 2; Length 151;
Best Local Similarity 45.3%; Pred. No. 6.3e-11;
Matches 58; Conservative 18; Mismatches 44; Indels 8; Gaps 3;

QY 1 QSGPLPKSLQALPSSLYPLEKPEVTLRCQPGPGVD--LYRLEKLS--SRYQD--QAV 52
DB 22 QAGHLPKPTLWAEPSGVIIQGSFVTLRCQSLQAEYHLYRENKASWVRRIQEPKNGQ 81
QY 53 LFIAMKRSLAGRYCSYQNGSLWLSLPDQLSLVATGVFAKPSLSAQPGPAYSSGGDVTL 112
DB 82 FPIPSITWEHAGRYHCQYVSHNSSEYSDPLELVVTGAYSKPTLSALPSPVVTLGQVTL 141
QY 113 QCQTRYGF 120
DB 142 QCVSQVAF 149

```

Search completed: October 29, 2005, 03:46:54  
Job time : 177 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 31, 2005, 17:55:59 ; Search time 163 Seconds  
(without alignments)  
106.774 Million cell updates/sec

Title: US-09-503-387-3\_COPY\_44\_88

Perfect score: 234

Sequence: 1 VTLRCQPPGVDLRLXKLS.....DQAVLFTPMKRSIAGRYRC 45

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 918587

Minimum DB seq length: 0

Maximum DB seq length: 46

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A\_Geneseq\_16Dec04:\*

1: geneseqp1980s:\*

2: geneseqp1990s:\*

3: geneseqp2000s:\*

4: geneseqp2001s:\*

5: geneseqp2002s:\*

6: geneseqp2003as:\*

7: geneseqp2003bs:\*

8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution..

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	216	92.3	41	4	AAB61258 Human TAN
2	216	92.3	41	6	ABU11224 Human TAN
3	164	70.1	41	4	AAB61271 Mouse TAN
4	164	70.1	41	6	ABU11237 Mouse TAN
5	81	34.6	19	4	AAV72805 Human pla
6	80	34.2	19	4	AAV72798 Human pla
7	69	29.5	19	4	AAV72806 Human pla
8	50	21.4	30	7	ADM35213 Human LY1
9	50	21.4	34	7	ADM34375 Human LY1
10	49	20.9	15	2	AAW78266 Fragment
11	46.5	19.9	45	4	AAW78266 Fragment
12	46.5	19.9	45	6	AAW78266 Fragment
13	45.5	19.4	37	3	AAV76375 Fragment
14	45.5	19.4	37	7	AAV76375 Fragment
15	43	18.4	30	7	ADM35214 Human LY1
16	43	18.4	34	7	ADM35214 Human LY1
17	43	18.4	35	7	ADM35214 Human LY1
18	43	18.4	35	7	ADM35214 Human LY1
19	43	18.4	36	7	ADM35214 Human LY1
20	43	18.4	36	7	ADM35214 Human LY1
21	43	18.4	36	7	ADM35214 Human LY1
22	43	18.4	37	7	ADM35214 Human LY1
23	43	18.4	37	7	ADM35214 Human LY1
24	43	18.4	37	7	ADM35214 Human LY1
25	43	18.4	38	7	ADM35214 Human LY1

26	43	18.4	38	7	ADF23085	Adf23085 Bioactive
27	43	18.4	39	7	ADF18773	Adf18773 Bioactive
28	43	17.9	36	7	ADF22973	Adf22973 Bioactive
29	42	17.9	37	7	ADF23069	Adf23069 Bioactive
30	42	17.9	38	7	ADF23133	Adf23133 Bioactive
31	42	17.9	39	7	ADF18789	Adf18789 Bioactive
32	41.5	17.7	41	4	ABO03192	ABO03192 Human mus
33	41.5	17.7	41	6	ABU12486	Abu12486 Novel hum
34	41.5	17.7	41	8	ADJ28512	Adj28512 Human mus
35	41	17.5	20	4	AAV72797	AAV72797 Human pla
36	41	17.5	30	3	AAO06160	AAO06160 Arabidops
37	41	17.5	30	5	AAU85099	AAU85099 Human TRP
38	41	17.5	30	8	ADS33495	CMET-HGF
39	40	17.5	33	7	ADF22690	Bioactive
40	41	17.5	34	7	ADF22083	Adf22083 Bioactive
41	41	17.5	34	7	ADF22177	Adf22177 Bioactive
42	41	17.5	35	7	ADF22024	Adf22024 Bioactive
43	41	17.5	35	7	ADF21988	Adf21988 Bioactive
44	41	17.5	35	7	ADF21926	Adf21926 Bioactive
45	41	17.5	35	7	ADF21866	Adf21866 Bioactive
46	41	17.5	36	7	ADF22929	Adf22929 Bioactive
47	41	17.5	36	7	ADF22941	Adf22941 Bioactive
48	41	17.5	36	7	ADF21914	Adf21914 Bioactive
49	41	17.5	36	7	ADF22897	Adf22897 Bioactive
50	41	17.5	36	7	ADF22961	Adf22961 Bioactive
51	41	17.5	37	7	ADF23057	Adf23057 Bioactive
52	41	17.5	37	7	ADF23025	Adf23025 Bioactive
53	41	17.5	37	7	ADF23037	Adf23037 Bioactive
54	41	17.5	37	7	ADF22993	Adf22993 Bioactive
55	41	17.5	38	7	ADF23089	Adf23089 Bioactive
56	41	17.5	38	7	ADF23121	Adf23121 Bioactive
57	41	17.5	38	7	ADF23101	Adf23101 Bioactive
58	41	17.5	39	7	ADF18777	Adf18777 Bioactive
59	40.5	17.3	43	8	ADK01832	Adk01832 Hepatitis
60	40	17.1	30	8	ADS33636	CMET-HGF
61	40	17.1	34	7	ADF22095	Bioactive
62	40	17.1	35	7	ADF22036	Bioactive
63	40	17.1	36	7	ADF22909	Bioactive
64	40	17.1	36	7	ADF22977	Bioactive
65	40	17.1	37	7	ADF23073	Adf23073 Bioactive
66	40	17.1	37	7	ADF23005	Adf23005 Bioactive
67	40	17.1	38	7	ADF23137	Adf23137 Bioactive
68	40	17.1	39	7	ADF18793	Adf18793 Bioactive
69	39	16.7	25	5	AAE20922	Peptide c
70	39	16.7	30	8	ADS33678	CMET-HGF
71	39	16.7	30	8	ADS33643	CMET-HGF
72	39	16.7	30	8	ADS33756	CMET-HGF
73	39	16.7	32	8	ABO57464	Human gen
74	39	16.7	33	7	ADF22694	Bioactive
75	39	16.7	34	7	ADF22181	Adf22181 Bioactive
76	39	16.7	34	7	ADF22071	Adf22071 Bioactive
77	39	16.7	35	7	ADF22044	Adf22044 Bioactive
78	39	16.7	35	7	ADF21992	Adf21992 Bioactive
79	39	16.7	35	7	ADF22012	Adf22012 Bioactive
80	39	16.7	35	7	ADF21870	Adf21870 Bioactive
81	39	16.7	36	7	ADF22945	Adf22945 Bioactive
82	39	16.7	36	7	ADF21918	Adf21918 Bioactive
83	39	16.7	36	7	ADF22885	Adf22885 Bioactive
84	39	16.7	36	7	ADF22917	Adf22917 Bioactive
85	39	16.7	36	7	ADF22949	Adf22949 Bioactive
86	39	16.7	37	7	ADF23045	Adf23045 Bioactive
87	39	16.7	37	7	ADF22981	Adf22981 Bioactive
88	39	16.7	37	7	ADF23013	Adf23013 Bioactive
89	39	16.7	37	7	ADF23041	Adf23041 Bioactive
90	39	16.7	38	7	ADF23077	Adf23077 Bioactive
91	39	16.7	38	7	ADF23109	Adf23109 Bioactive
92	39	16.7	38	7	ADF23105	Adf23105 Bioactive
93	39	16.7	38	8	ABO54671	Human gen
94	39	16.7	39	7	ADF18765	Adf18765 Bioactive
95	39	16.7	41	3	AAB34631	Gene 2 hu
96	39	16.7	41	3	AAB34632	Human sec
97	39	16.7	42	4	ABO03229	Human mus
98	39	16.7	42	4	AAE13010	Consensus

99 39 16.7 42 6 ABU12523 Novel hum  
100 39 16.7 42 8 ADJ28549 Human mus

ALIGNMENTS

RESULT 1  
AAB61258  
ID AAB61258 standard; protein; 41 AA.  
AC AAB61258;  
XX  
XX  
DT 04-APR-2001 (first entry)  
DE Human TANGO 268 Ig-like domain #1.  
XX  
XX  
KW Human; TANGO 268; cardiant; cerebroprotective; cytostatic; anticoagulant;  
KW thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI;  
KW platelet membrane glycoprotein receptor; bleeding disorder;  
KW blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;  
KW ischaemia; cardiovascular disease; immunological disease; liver disorder;  
KW cancer.  
XX  
XX  
OS Homo sapiens.  
XX  
XX  
PN WO200100810-A1.  
XX  
PD 04-JAN-2001.  
XX  
XX  
PF 30-JUN-2000; 2000WO-US018152.  
XX  
XX  
PR 30-JUN-1999; 99US-00345468.  
PR 06-DEC-1999; 99US-00454824.  
PR 14-FEB-2000; 2000US-00503387.  
XX  
XX  
PA (MILL-) MILLENNIUM PHARM INC.  
XX  
XX  
PI Busfield SJ, Villeval J, Jandrot-Perrus M, Vainchencker W;  
PI Gill DS, Qian MD, Kingsbury G;  
XX  
XX  
DR WPI; 2001-080877/09.  
XX  
XX  
PT New genes encoding human platelet-expressed collagen receptor.  
PT glycoprotein VI, and its modulators, useful for preventing, treating and  
PT diagnosing hemorrhagic disorders, thrombotic diseases and immunological  
PT disorders.  
XX  
XX  
PS Disclosure; Page 203; 227pp; English.  
XX  
XX  
CC The present sequence is given in a specification relating to an isolated  
CC nucleic acid molecule encoding a platelet membrane glycoprotein receptor  
CC glycoprotein VI (GPVI), also called TANGO 268. The GPVI polynucleotides  
CC and polypeptides and their modulators, e.g. antisense nucleic acids,  
CC ribozymes and antibodies, are useful for preventing, treating and  
CC diagnosing disorders associated with aberrant expression or activity of  
CC GPVI. These disorders include bleeding disorders (e.g.  
CC thrombocytopaenia), blood vessel injury, thrombotic disorders (e.g.  
CC thrombotic occlusion of the coronary arteries), haemorrhagic disorders,  
CC coronary artery and cerebral artery diseases (e.g. stroke and ischaemia),  
CC cardiovascular diseases (e.g. atherosclerosis and myocardial infarction),  
CC immunological diseases (e.g. platelet disorder) and embryonic liver  
CC disorders. Preferably they are used to prevent acute cardiac ischaemia  
CC following angioplasty and metastatic cancers, especially of the colon and  
CC liver  
XX  
SQ Sequence 41 AA;  
Query Match 92.3%; Score 216; DB 4; Length 41;  
Best Local Similarity 100.0%; Pred. No. 1.2e-23;  
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 CQGPVVDLYRLEKLSRRYQDQAVLFIPMKRSLAGRYRC 45

1 CQGPVVDLYRLEKLSRRYQDQAVLFIPMKRSLAGRYRC 41

Db

RESULT 2

ABU11224  
ID ABU11224 standard; peptide; 41 AA.  
XX  
XX  
AC ABU11224;  
XX  
XX  
DT 06-FEB-2003 (first entry)  
DE Human TANGO 268 Ig-like domain #1.  
XX  
XX  
KW Human; mouse; variable heavy; VH; antigen: cancer;  
KW complementarity determining region; TANGO 268; glycoprotein VI; GPVI;  
KW TANGO 268; extracellular matrix; collagen; platelet release;  
KW proliferation; migration; embryogenesis; inflammation; thrombosis;  
KW degradation; thrombocytopaenia; antibody; thrombotic disorder;  
KW cerebral vascular disease; stroke; ischaemia; venous thromboembolism;  
KW leg swelling; pain; ulceration; pulmonary embolism; coronary disease;  
KW cardiovascular disease; angina pectoris; myocardial infarction;  
KW coronary restenosis; atherosclerosis; immunological disorder;  
KW developmental disorder; embryonic disorder; liver disorder;  
KW cerebral vascular disease; venous thromboembolism disease.  
XX  
XX  
OS Homo sapiens.  
XX  
XX  
PN WO200280968-A1.  
XX  
XX  
PD 17-OCT-2002.  
XX  
XX  
PF 09-APR-2002; 2002WO-US011122.  
XX  
XX  
PR 09-APR-2001; 2001US-00829495.  
XX  
XX  
PA (MILL-) MILLENNIUM PHARM INC.  
XX  
XX  
PI Busfield SJ, Villeval J, Jandrot-Perrus M, Vainchencker W;  
PI Gill DS, Qian DM, Kingsbury G;  
XX  
XX  
DR WPI; 2003-058477/05.  
XX  
XX  
PT Novel substantially purified antibody immunospecifically binding to TANGO  
PT 268 antigen, useful for treating bleeding disorders such as  
PT thrombocytopaenia, stroke, ischemia, pulmonary embolism, atherosclerosis.  
XX  
XX  
PS Disclosure; Page 212; 236pp; English.  
XX  
XX  
CC This invention relates to a novel purified antibody comprising a variable  
CC heavy (VH) complementarity determining region (CDR1, CDR2 or VH CDR3;  
CC or variable light (VL) CDR1, VL CDR2 or VL CDR3, and immunospecifically  
CC binding to a TANGO 268 (also referred as glycoprotein VI (GPVI)) antigen.  
CC The antibodies of the invention act to decrease or block TANGO 268  
CC binding to extracellular matrix components, or as a Collagen or platelet  
CC release and aggregation blocker. The antibodies of the invention are  
CC useful for modulating proliferation, migration, morphology  
CC differentiation and/or function of megakaryocytes and platelets,  
CC including during development e.g. embryogenesis, modulating leukocyte-  
CC platelet and platelet-endothelium interactions in inflammation and/or  
CC thrombosis, and modulating platelet aggregation and degradation. They  
CC are also useful for modulating disorders associated with abnormal or  
CC aberrant megakaryocyte and/or platelet proliferation, migration,  
CC morphology, differentiation and/or function, e.g. bleeding disorders such  
CC as thrombocytopaenia. Other diseases which may be modulated by these  
CC antibodies are thrombotic disorders, cerebral vascular diseases (e.g.  
CC stroke and ischaemia) venous thromboembolism diseases (e.g. diseases  
CC involving leg swelling, pain and ulceration, pulmonary embolism, etc);  
CC coronary diseases (e.g. cardiovascular diseases including angina  
CC pectoris, myocardial infarction, coronary restenosis, atherosclerosis,  
CC etc); immunological disorders, developmental disorders, embryonic  
CC disorders, liver disorders, cerebral vascular diseases, venous  
CC thromboembolism disease, coronary diseases, and metastatic cancers. The



CC antibodies of the invention only causes a transient decrease in platelet  
CC counts, platelet aggregation, and/or platelet activation and so have some  
CC advantages over prior art methods. The present sequence represents a  
CC peptide sequence used to generate the antibodies of the invention  
XX  
SQ Sequence 41 AA;

Query Match 92.3%; Score 216; DB 6; Length 41;  
Best Local Similarity 100.0%; Pred. No. 1.2e-23;  
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 CQGPVGLYRLEKLSRSSRYQDQAVLFTIPAMKRSIAGRYRC 45  
Db 1 CQGPVGLYRLEKLSRSSRYQDQAVLFTIPAMKRSIAGRYRC 41

RESULT 3  
AAB61271  
ID AAB61271 standard; protein; 41 AA.

AC AAB61271;

XX 04-APR-2001 (first entry)

DT Mouse TANGO 268 Ig-like domain #1.

XX Mouse; TANGO 268; cardiant; cerebroprotective; cytostatic; anticoagulant;  
XX thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI;  
XX platelet membrane glycoprotein receptor; bleeding disorder;  
XX blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;  
XX ischaemia; cardiovascular disease; immunological disease; liver disorder;  
XX cancer.

XX Mus musculus.

XX WO200100810-A1.

PN 04-JAN-2001.

PD 30-JUN-2000; 2000WO-US018152.

PF 30-JUN-1999; 99US-00345468.

PR 06-DEC-1999; 99US-00454824.

PR 14-FEB-2000; 2000US-00503387.

XX (MILL-) MILLENNIUM PHARM INC.

XX Busfield SJ, Villelval J, Jandrot-Perrus M, Vainchencker W;

PI Gill DS, Qian MD, Kingsbury G;

XX WPI; 2001-080877/09.

XX New genes encoding human platelet-expressed collagen receptor,  
PT glycoprotein VI, and its modulators, useful for preventing, treating and  
PT diagnosing hemorrhagic disorders, thrombotic diseases and immunological  
PT disorders.

PS Disclosure; Page 210; 227pp; English.

XX The present sequence is given in a specification relating to an isolated  
CC nucleic acid molecule encoding a platelet membrane glycoprotein receptor  
CC glycoprotein VI (GPVI), also called TANGO 268. The GPVI polynucleotides  
CC and polypeptides and their modulators, e.g. antisense nucleic acids,  
CC ribozymes and antibodies, are useful for preventing, treating and  
CC diagnosing disorders associated with aberrant expression or activity of  
CC GPVI. These disorders include bleeding disorders (e.g.  
CC thrombocytopenia), blood vessel injury, thrombotic disorders (e.g.  
CC thrombotic occlusion of the coronary arteries), haemorrhagic disorders,  
CC coronary artery and cerebral artery diseases (e.g. stroke and ischaemia),  
CC cardiovascular diseases (e.g. atherosclerosis and myocardial infarction),  
CC immunological diseases (e.g. platelet disorder) and embryonic liver  
CC disorders. Preferably they are used to prevent acute cardiac ischaemia  
CC following angioplasty and metastatic cancers, especially of the colon and

CC liver  
XX  
SQ Sequence 41 AA;

Query Match 70.1%; Score 164; DB 4; Length 41;  
Best Local Similarity 73.2%; Pred. No. 4.5e-16;  
Matches 30; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Oy 5 CQGPVGLYRLEKLSRSSRYQDQAVLFTIPAMKRSIAGRYRC 45  
Db 1 CQGPVGLYRLEKLSRSSRYQDQAVLFTIPAMKRSIAGRYRC 41

RESULT 4  
ABU11237

ID ABU11237 standard; peptide; 41 AA.

AC ABU11237;

DT 06-FEB-2003 (first entry)

DE Mouse TANGO 268 IgG-like domain.

XX Human; mouse; variable heavy; VH; antigen; cancer;  
XX complementarity determining region; TANGO 268; glycoprotein VI; GPVI;  
XX TANGO 268; extracellular matrix; collagen; platelet release;  
XX proliferation; migration; embryogenesis; inflammation; thrombosis;  
XX degradation; thrombocytopenia; antibody; thrombotic disorder;  
XX cerebral vascular disease; stroke; ischaemia; venous thromboembolism;  
XX leg swelling; pain; ulceration; pulmonary embolism; coronary disease;  
XX cardiovascular disease; angina pectoris; myocardial infarction;  
XX coronary restenosis; atherosclerosis; immunological disorder;  
XX developmental disorder; embryonic disorder; liver disorder;  
XX cerebral vascular disease; venous thromboembolism disease.

XX Mus musculus.

XX WO200280968-A1.

XX 17-OCT-2002.

XX 09-APR-2002; 2002WO-US011122.

XX 09-APR-2001; 2001US-00829495.

XX (MILL-) MILLENNIUM PHARM INC.

XX Busfield SJ, Villelval J, Jandrot-Perrus M, Vainchencker W;

PI Gill DS, Qian DM, Kingsbury G;

XX WPI; 2003-058477/05.

XX Novel substantially purified antibody immunospecifically binding to TANGO  
PT 268 antigen, useful for treating bleeding disorders such as  
PT thrombocytopenia, stroke, ischemia, pulmonary embolism, atherosclerosis.

PS Disclosure; Page 219; 236pp; English.

XX This invention relates to a novel purified antibody comprising a variable  
CC heavy (VH) complementarity determining region (CDR)1, VH CDR2 or VH CDR3;  
CC or variable light (VL) CDR1, VL CDR2 or VL CDR3, and immunospecifically  
CC binding to a TANGO 268 (also referred as glycoprotein VI (GPVI)) antigen.  
CC The antibodies of the invention act to decrease or block TANGO 268  
CC binding to extracellular matrix components, or as a collagen or platelet  
CC release and aggregation blocker. The antibodies of the invention are  
CC useful for modulating proliferation, migration, morphology,  
CC differentiation and/or function of megakaryocytes and platelets,  
CC including during development e.g. embryogenesis, modulating leukocyte-  
CC platelet and platelet-endothelium interactions in inflammation and/or  
CC thrombosis, and modulating platelet aggregation and degradation. They  
CC are also useful for modulating disorders associated with abnormal or  
CC aberrant megakaryocyte and/or platelet proliferation, migration,  
CC morphology, differentiation and/or function, e.g. bleeding disorders such



AC AAY72806;  
DT 31-MAY-2001 (first entry)  
DE Human platelet membrane glycoprotein VI (GPVI) peptide 12.  
KW Human; platelet membrane glycoprotein VI; GPVI; thrombolytic; therapy;  
XX vascular disease; thrombosis.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT Misc-difference 4 /label= Unknown  
FT Misc-difference 5 /label= Unknown  
FT WO200116321-A1.  
PN 08-MAR-2001.  
PD  
PF 01-SEP-2000; 200WO-US023975.  
PR 01-SEP-1999; 99US-0152197P.  
PR 08-OCT-1999; 99US-0158251P.  
XX (SAKA ) OTSUKA PHARM CO LTD.  
PA Tandon N, Sun B, Nakamura T, Yamamoto N;  
PI WPI; 2001-226691/23.  
DR  
XX Anti-thrombotic medicament, comprising a polypeptide having the  
PT extracellular domain of platelet membrane glycoprotein VI or its variant,  
PT useful for treating a vascular disease and reducing platelet activation.  
XX Disclosure; Page 17; 74pp; English.  
PS  
CC The present sequence is a human platelet membrane glycoprotein VI (GPVI)  
CC peptide 12. The medicament comprising GPVI is useful for treating  
CC vascular disease, and for reducing platelet activation which involves  
CC contacting platelets with the medicament. The extracellular portion of  
CC GPVI is used therapeutically to attenuate platelet activation and  
CC aggregation and to treat thrombosis and other vascular diseases.  
CC Antibodies generated against GPVI are used as research and  
CC immunotherapeutic agents  
XX  
SQ Sequence 19 AA;  
Query Match 29.5%; Score 69; DB 4; Length 19;  
Best Local Similarity 73.7%; Pred. No. 0.013;  
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 18 KLSSRRYQDQAVLIPAMK 36  
DB 1 KLDXXRYQDQAVLIPAMK 19  
RESULT 8  
ADM35213  
ID ADM35213 standard; peptide; 30 AA.  
XX  
AC ADM35213;  
XX  
DT 03-JUN-2004 (first entry)  
DE Human LY1448P cancer related peptide for cancer detection method.  
XX  
KW cytostatic; T-cell vaccine; detection; cancer;  
KW chronic lymphocytic leukemia.  
XX  
OS Homo sapiens.  
XX

PN WO2003077836-A2.  
XX 25-SEP-2003.  
XX 06-NOV-2002; 2002WO-US035728.  
XX 06-NOV-2001; 2001US-00040862.  
PR 23-MAY-2002; 2002US-00154884.  
XX (CORI-) CORIXA CORP.  
XX Gaiger A, Algate PA, Mannion J, Retter M;  
PI WPI; 2003-756941/71.  
XX  
PT Detecting cancer in a patient comprises contacting a biological sample  
PT from the patient with a binding agent that binds to a cancer-associated  
PT polypeptide and comparing the amount of polypeptide to a predetermined  
PT cutoff value.  
XX  
PS Disclosure; SEQ ID NO 10438; 419pp; English.  
XX  
CC The invention relates to a method of detecting (M1) cancer in a patient  
CC by: (i) contacting a biological sample from the patient with an agent  
CC that binds to any of three polypeptides given in the specification; (ii)  
CC detecting in a sample an amount of the peptide that binds to the binding  
CC agent; and (iii) comparing the amount of polypeptide present in the  
CC patient's sample to a predetermined cutoff value. The specification also  
CC discloses a separate method for detecting (M2) cancer in a patient by a  
CC method similar to M1, except that the detection agent is an  
CC oligonucleotide that binds to any of three polynucleotides given in the  
CC specification. M1 and M2 are useful for detecting the presence of cancer  
CC in a patient, especially chronic lymphocytic leukemia. The applicants  
CC have identified specific human polypeptides overexpressed in one or more  
CC types of hematological malignancies. This sequence corresponds to a  
CC peptide used in the method of the invention.  
XX  
SQ Sequence 30 AA;  
Query Match 21.4%; Score 50; DB 7; Length 30;  
Best Local Similarity 61.1%; Pred. No. 13;  
Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
QY 28 AVLFIIPAMKSLAGRYRC 45  
DB 11 AELEIPAVKSDAGKYVC 28  
RESULT 9  
ADM34375  
ID ADM34375 standard; peptide; 34 AA.  
XX  
AC ADM34375;  
XX  
DT 03-JUN-2004 (first entry)  
DE Human LY1448P cancer related peptide for cancer detection method.  
XX  
KW cytostatic; T-cell vaccine; detection; cancer;  
KW chronic lymphocytic leukemia.  
XX  
OS Homo sapiens.  
XX  
PN WO2003077836-A2.  
XX  
PD 25-SEP-2003.  
XX  
PF 06-NOV-2002; 2002WO-US035728.  
XX  
PR 06-NOV-2001; 2001US-00040862.  
PR 23-MAY-2002; 2002US-00154884.  
XX (CORI-) CORIXA CORP.  
XX



KW antiarthritic; neuroprotective; dermatological; immunosuppressive;  
 KW antiinflammatory; antiasthmatic; antiulcer; antianaemic; hepatotropic.  
 OS Homo sapiens.  
 XX WO200172827-A2.  
 XX 04-OCT-2001.  
 XX 23-MAR-2001; 2001WO-US009470.  
 XX 24-MAR-2000; 2000US-0191863P.  
 XX (MILL-) MILLENNIUM PHARM INC.  
 XX Glucksmann MA;  
 PI WIPI; 2001-626254/72.  
 DR New polypeptide for preventing or treating disorders associated with  
 PT cellular adhesion, proliferation or differentiation, comprises  
 PT polypeptide 33395, a member of the leucine rich repeat protein family.  
 XX Disclosure; Fig 4A-B; 133pp; English.  
 XX The invention provides an isolated nucleic acid encoding a polypeptide of  
 CC the leucine rich repeat (LRR) family, designated 33395. The 33395  
 CC polypeptide can be expressed by standard recombinant methodology. The  
 CC 33395 polynucleotides and polypeptide can be used to prevent or treat  
 CC disorders associated with 33395 expression, for example those involving  
 CC aberrant cellular adhesion, proliferation or differentiation. Specific  
 CC examples include melanoma, juvenile AIDS, diabetes mellitus,  
 CC rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis,  
 CC Chron's disease, ulcerative colitis, asthma, anemia, and chronic active  
 CC hepatitis. Sequences AAC5815-817 represent consensus amino acid  
 CC sequences derived from a hidden Markov model corresponding to the  
 CC immunoglobulin domains of the the human 33395 polypeptide  
 XX Sequence 45 AA;  
 SQ  
 Query Match 19.9%; Score 46.5; DB 4; Length 45;  
 Best Local Similarity 34.7%; Pred. No. 67;  
 Matches 17; Conservative 0; Mismatches 19; Indels 13; Gaps 2;  
 QY 1 VTLCRCQ----GPPGVDLVRLKLSRRYQDQAVLFIPAMKRLAGRYRC 45  
 Db 4 VTLCVSVGFGPPPTVLRNGKLS-----LTISVTPEDSGGYTC 43  
 RESULT 12  
 AAE35359  
 ID AAE35359 standard; protein; 45 AA.  
 XX AAE35359;  
 AC  
 XX 17-JUN-2003 (first entry)  
 DT Human protein related to the invention.  
 DE  
 XX Human; sodium channel beta-4 subunit; 98359 protein; gene therapy; AIDS;  
 KW shock; hypertension; psychiatric disease; obsessive-compulsive disorder;  
 KW bipolar affective disorder; attention deficit disorder; phobic disorder;  
 KW cardiovascular disorder; neurological disorder; spinocerebellar ataxia;  
 KW Alzheimer's disease; Parkinson's disease; Tourette's syndrome; anxiety;  
 KW autoimmune disorder; cellular proliferative disorder; Krabbe's disease;  
 KW metabolic disorder; multiple sclerosis; cardiomyopathy; liver disorder;  
 KW bone metabolism disorder; endothelial cell disorder; viral encephalitis;  
 KW acquired immune deficiency syndrome; peripheral neuropathy; arrhythmia;  
 KW poliomyelitis; demyelinating disease; leukodystrophy; epilepsy; cancer;  
 KW dementia; Leigh disease; heart failure; diabetes; arthritis; rabies;  
 KW pain.  
 XX Homo sapiens.  
 OS

XX EP1258495-A1.  
 XX 20-NOV-2002.  
 XX 09-MAY-2002; 2002EP-00253262.  
 XX 09-MAY-2001; 2001US-0289893P.  
 XX (MILL-) MILLENNIUM PHARM INC.  
 XX Curtis RAJ;  
 PI WIPI; 2003-185859/19.  
 DR New isolated human sodium channel beta-4 subunit nucleic acid molecule  
 PT and polypeptide, useful for diagnosing and treating disorders with  
 PT aberrant beta-4 subunit function or expression, such as neurological and  
 PT cardiovascular diseases.  
 XX Disclosure; Page 51; 62pp; English.  
 XX The invention relates to human sodium channel beta-4 subunit, 98359  
 CC polypeptides and polynucleotides. The methods and compositions of the  
 CC invention are useful for diagnosing, screening and treating disorders  
 CC associated with aberrant or deficient sodium channel beta-4 subunit  
 CC function or expression such as paramyotonia congenital, hyperkalaemic  
 CC periodic paralysis, epilepsy, psychiatric diseases (anxiety or phobic  
 CC disorders, attention deficit disorder, obsessive-compulsive disorder and  
 CC bipolar affective disorder), dementia, cardiovascular disorders  
 CC (hypertension, shock, heart failure, arrhythmias and cardiomyopathy),  
 CC neurological disorders (Alzheimer's or Parkinson's disease,  
 CC spinocerebellar ataxia and Tourette's syndrome), autoimmune disorders  
 CC (diabetes, arthritis), cellular proliferative disorders (cancer), bone  
 CC metabolism disorders, liver disorders, viral infections (AIDS), rabies,  
 CC herpes simplex, poliomyelitis, viral encephalitis and peripheral  
 CC neuropathy), endothelial cell disorders, demyelinating diseases (multiple  
 CC sclerosis), pain and/or metabolic disorders (Leukodystrophies, Krabbe's  
 CC disease and Leigh disease). Polynucleotides of the invention are used to  
 CC identify an individual from a biological sample (tissue typing), and in  
 CC forensic identification of a biological sample. The invention is useful  
 CC in gene therapy. The present sequence is human protein related to the  
 CC invention  
 XX Sequence 45 AA;  
 SQ  
 Query Match 19.9%; Score 46.5; DB 6; Length 45;  
 Best Local Similarity 34.7%; Pred. No. 67;  
 Matches 17; Conservative 0; Mismatches 19; Indels 13; Gaps 2;  
 QY 1 VTLCRCQ----GPPGVDLVRLKLSRRYQDQAVLFIPAMKRLAGRYRC 45  
 Db 4 VTLCVSVGFGPPPTVLRNGKLS-----LTISVTPEDSGGYTC 43  
 RESULT 13  
 AAV76375  
 ID AAV76375 standard; protein; 37 AA.  
 XX AAV76375;  
 AC  
 XX 23-MAR-2000 (first entry)  
 DT Fragment of human secreted protein encoded by gene 72.  
 DE  
 XX Human; secreted protein; cancer; tumour; developmental abnormality;  
 KW foetal deficiency; blood disorder; immune system disorder; inflammation;  
 KW autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;  
 KW schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;  
 KW atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;  
 KW digestive disorder; endocrine disorder; infection; AIDS; leukaemia;  
 KW therapy.  
 XX

OS Homo sapiens.  
XX WO9598660-A1.  
XX 18-NOV-1999.  
XX 06-MAY-1999; 99WO-US009847.  
XX 12-MAY-1998; 98US-0085093P.  
PR 12-MAY-1998; 98US-0085094P.  
PR 12-MAY-1998; 98US-0085105P.  
PR 12-MAY-1998; 98US-0085180P.  
PR 18-MAY-1998; 98US-0085906P.  
PR 18-MAY-1998; 98US-0085920P.  
PR 18-MAY-1998; 98US-0085921P.  
PR 18-MAY-1998; 98US-0085922P.  
PR 18-MAY-1998; 98US-0085923P.  
PR 18-MAY-1998; 98US-0085924P.  
PR 18-MAY-1998; 98US-0085925P.  
PR 18-MAY-1998; 98US-0085927P.  
PR 18-MAY-1998; 98US-0085928P.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX Ruben SM, Florence K, Ni J, Rosen CA, Carter KC, Moore PA;  
PI Olsen HS, Shi Y, Young PE, Wei F, Brewer LA, Soppet DR, Lafleur DW,  
PI Endress GA, Ebner R;  
XX WPI; 2000-062296/05.  
XX New isolated human genes and the secreted polypeptides they encode,  
PT useful for diagnosis and treatment of e.g. cancers, neurological  
PT disorders, immune diseases, inflammation or blood disorders.  
XX Disclosure; Page 460; 475pp; English.  
XX AZ65250 to AZ65350 represent 97 isolated human secreted protein genes.  
CC AAY76124 to AAY76223 are the secreted proteins encoded by the 97 human  
CC genes. This sequence represents a fragment of one of the human secreted  
CC proteins. The genes and their corresponding secreted polypeptides are  
CC useful for preventing, treating or ameliorating medical conditions, e.g.  
CC by protein or gene therapy. Also pathological conditions can be diagnosed  
CC by determining the amount of the new polypeptides in a sample or by  
CC determining the presence of mutations in the new genes. Specific uses are  
CC described for each of the 97 genes, based on which tissues they are most  
CC highly expressed in, and include developing products for the diagnosis or  
CC treatment of cancer, tumours, developmental abnormalities and foetal  
CC deficiencies, blood disorders, diseases of the immune system, autoimmune  
CC diseases, inflammation, allergies, Alzheimer's and cognitive disorders,  
CC schizophrenia, arthritis, asthma, psoriasis, sepsis, skin disorders,  
CC atherosclerosis, diabetes, cardiovascular disorders, kidney disorders,  
CC digestive/endocrine disorders, infections and AIDS. The polypeptides are  
CC also useful for identifying their binding partners. The sequences shown  
CC in AAY76224 to AAY76424 represent fragments of the secreted proteins  
XX  
SQ Sequence 37 AA;  
Query Match 19.4%; Score 45.5; DB 3; Length 37;  
Best Local Similarity 33.3%; Pred. No. 74;  
Matches 13; Conservative 2; Mismatches 13; Indels 11; Gaps 1;  
QY 7 GPGVDVLRLEKLSRSSYQDQAVLFIPAMKRSLAGRYRC 45  
Db 1 GPP-----SPRGLPSLPULHPAPRYLQSRVAC 28  
RESULT 14  
ADE12024  
ID ADE12024 standard; protein; 37 AA.  
XX  
AC ADE12024;  
XX  
PT 29-JAN-2004 (first entry)

XX Human secreted polypeptide #278.  
DE  
XX Secreted protein; cancer; liver disorder; hepatitis; neural disorder;  
KW Alzheimer's disease; human.  
XX Synthetic.  
OS Homo sapiens.  
XX US2003100051-A1.  
XX 29-MAY-2003.  
XX 10-SEP-2001; 2001US-00948783.  
XX 12-MAY-1998; 98US-0085093P.  
PR 12-MAY-1998; 98US-0085094P.  
PR 12-MAY-1998; 98US-0085105P.  
PR 12-MAY-1998; 98US-0085180P.  
PR 18-MAY-1998; 98US-0085906P.  
PR 18-MAY-1998; 98US-0085920P.  
PR 18-MAY-1998; 98US-0085921P.  
PR 18-MAY-1998; 98US-0085922P.  
PR 18-MAY-1998; 98US-0085923P.  
PR 18-MAY-1998; 98US-0085924P.  
PR 18-MAY-1998; 98US-0085925P.  
PR 18-MAY-1998; 98US-0085927P.  
PR 18-MAY-1998; 98US-0085928P.  
PR 06-MAY-1999; 99WO-US009847.  
PR 10-NOV-1999; 99US-00437658.  
PR 11-SEP-2000; 2000US-0231846P.  
PR 28-JUN-2001; 2001US-00892877.  
XX (RUBE/) RUBEN S M.  
PA (FLOR/) FLORENCE K A.  
PA (NIJ/) NI J.  
PA (ROSE/) ROSEN C A.  
PA (CART/) CARTER K C.  
PA (MOOR/) MOORE P A.  
PA (OLSE/) OLSEN H S.  
PA (SHIY/) SHI Y.  
PA (YOUN/) YOUNG P E.  
PA (WEIV/) WEI Y.  
PA (BREW/) BREWER L A.  
PA (SOPP/) SOPPET D R.  
PA (LAFLE/) LAFLEUR D W.  
PA (ENDR/) ENDRESS G A.  
PA (EBNE/) EBNER R.  
PA (BIRS/) BIRSE C E.  
XX Ruben SM, Florence KA, Ni J, Rosen CA, Carter KC, Moore PA;  
PI Olsen HS, Shi Y, Young PE, Wei Y, Brewer LA, Soppet DR, Lafleur DW;  
PI Endress GA, Ebner R, Birse CE;  
XX WPI; 2003-801210/75.  
XX New nucleic acid molecule, useful for preparing a medicament for  
PT preventing, treating or ameliorating a medical condition e.g. cancer,  
PT liver disorders or neural disorders.  
XX Claim 11; SEQ ID NO 396; 453pp; English.  
XX The invention relates to human secreted polypeptides and the  
CC polynucleotides encoding them. The sequences are useful for preparing  
CC medicaments for preventing, treating or ameliorating medical conditions  
CC e.g., cancer, liver disorders such as hepatitis or neural disorders such  
CC as Alzheimer's disease. This sequence represents a human secreted  
CC polypeptide of the invention.  
XX  
SQ Sequence 37 AA;  
Query Match 19.4%; Score 45.5; DB 7; Length 37;  
Best Local Similarity 33.3%; Pred. No. 74;



KW keratin; dermal fibroblast; epithelial tissue; cytokine-like activity;  
 KW antiinflammatory; antiulcer; vulnerary; analgesic;  
 KW cell proliferation activator; deodourant; cleanser; toenail care;  
 KW sunburn; puncture wound; Crohn's disease; skin graft; diabetic ulcer.  
 OS Unidentified.  
 XX WO2003064449-A2.  
 PN 07-AUG-2003.  
 PD 28-JAN-2003; 2003WO-US002645.  
 XX 28-JAN-2002; 2002US-0352396P.  
 PF (KERA-) KERAPLAST TECHNOLOGIES INC.  
 XX Cowsar DR;  
 PI WPI; 2003-812322/76.  
 DR Composition comprising an isolated bioactive keratin peptides useful for  
 PT cosmetic preparation, and treating conditions involving damaged, aged and  
 PT diseased epithelial tissue and skin.  
 XX Disclosure; SEQ ID NO 5927; 158pp; English.  
 PS This invention relates to a novel composition comprising an isolated  
 CC bioactive keratin peptide of 4-39 amino acids in length. Specifically, it  
 CC refers to keratin proteins that can stimulate the growth of dermal  
 CC fibroblasts for use in treating damaged, aged or diseased epithelial  
 CC tissue and skin. Furthermore, they exhibit cytokine-like activity,  
 CC particularly cell differentiation, adhesion and migration, and in  
 CC combination with other growth factors can be used to enhance the healing  
 CC activity of damaged skin or bone tissue. The present invention describes  
 CC these peptides as antiinflammatory, antiulcer, vulnerary, analgesic and  
 CC cell proliferation activators. Accordingly, there are various  
 CC applications for cosmetics e.g. deodourant, cleanser and toenail care  
 CC compositions, also in topical applications to damaged epithelial tissue  
 CC from sunburn, ulcers or puncture wounds so as to relieve pain, burning or  
 CC itching. The compositions can further be used to treat Crohn's disease,  
 CC skin grafts or diabetic ulcers. This peptide sequence, derived from human  
 CC hair or sheep wool keratin proteins, is a biologically active keratin  
 CC peptide of the invention.  
 XX Sequence 35 AA;  
 SQ Query Match 18.4%; Score 43; DB 7; Length 35;  
 Best Local Similarity 35.3%; Pred. No. 1.6e+02;  
 Matches 12; Conservative 4; Mismatches 8; Indels 10; Gaps 1;  
 QY 2 TLRCQ-----GPPGVLDLYRLEKLSRRYQ 25  
 ||||| | ||| : : : :  
 Db 1 TLRCQLGRLNVEVDAAPTVDLNRVLNSTRSQYE 34  
 RESULT 18  
 ADF22020  
 ID ADF22020 standard; peptide; 35 AA.  
 AC ADF22020;  
 XX 12-FEB-2004 (first entry)  
 DT Bioactive keratin peptide (SeqID 5895).  
 XX keratin; dermal fibroblast; epithelial tissue; cytokine-like activity;  
 KW antiinflammatory; antiulcer; vulnerary; analgesic;  
 KW cell proliferation activator; deodourant; cleanser; toenail care;  
 KW sunburn; puncture wound; Crohn's disease; skin graft; diabetic ulcer.  
 XX Unidentified.  
 OS WO2003064449-A2.  
 PN 07-AUG-2003.  
 PD 28-JAN-2003; 2003WO-US002645.  
 XX 28-JAN-2002; 2002US-0352396P.  
 PF (KERA-) KERAPLAST TECHNOLOGIES INC.  
 XX Cowsar DR;  
 PI WPI; 2003-812322/76.  
 DR Composition comprising an isolated bioactive keratin peptides useful for  
 PT cosmetic preparation, and treating conditions involving damaged, aged and  
 PT diseased epithelial tissue and skin.  
 XX Disclosure; SEQ ID NO 5927; 158pp; English.  
 PS This invention relates to a novel composition comprising an isolated  
 CC bioactive keratin peptide of 4-39 amino acids in length. Specifically, it  
 CC refers to keratin proteins that can stimulate the growth of dermal  
 CC fibroblasts for use in treating damaged, aged or diseased epithelial  
 CC tissue and skin. Furthermore, they exhibit cytokine-like activity,  
 CC particularly cell differentiation, adhesion and migration, and in  
 CC combination with other growth factors can be used to enhance the healing  
 CC activity of damaged skin or bone tissue. The present invention describes  
 CC these peptides as antiinflammatory, antiulcer, vulnerary, analgesic and  
 CC cell proliferation activators. Accordingly, there are various  
 CC applications for cosmetics e.g. deodourant, cleanser and toenail care  
 CC compositions, also in topical applications to damaged epithelial tissue  
 CC from sunburn, ulcers or puncture wounds so as to relieve pain, burning or  
 CC itching. The compositions can further be used to treat Crohn's disease,  
 CC skin grafts or diabetic ulcers. This peptide sequence, derived from human  
 CC hair or sheep wool keratin proteins, is a biologically active keratin  
 CC peptide of the invention.  
 XX Sequence 35 AA;  
 SQ Query Match 18.4%; Score 43; DB 7; Length 35;  
 Best Local Similarity 35.3%; Pred. No. 1.6e+02;  
 Matches 12; Conservative 4; Mismatches 8; Indels 10; Gaps 1;

PN WO2003064449-A2.  
 XX 07-AUG-2003.  
 PD 28-JAN-2003; 2003WO-US002645.  
 XX 28-JAN-2002; 2002US-0352396P.  
 PF (KERA-) KERAPLAST TECHNOLOGIES INC.  
 XX Cowsar DR;  
 PI WPI; 2003-812322/76.  
 DR Composition comprising an isolated bioactive keratin peptides useful for  
 PT cosmetic preparation, and treating conditions involving damaged, aged and  
 PT diseased epithelial tissue and skin.  
 XX Disclosure; SEQ ID NO 5895; 158pp; English.  
 PS This invention relates to a novel composition comprising an isolated  
 CC bioactive keratin peptide of 4-39 amino acids in length. Specifically, it  
 CC refers to keratin proteins that can stimulate the growth of dermal  
 CC fibroblasts for use in treating damaged, aged or diseased epithelial  
 CC tissue and skin. Furthermore, they exhibit cytokine-like activity,  
 CC particularly cell differentiation, adhesion and migration, and in  
 CC combination with other growth factors can be used to enhance the healing  
 CC activity of damaged skin or bone tissue. The present invention describes  
 CC these peptides as antiinflammatory, antiulcer, vulnerary, analgesic and  
 CC cell proliferation activators. Accordingly, there are various  
 CC applications for cosmetics e.g. deodourant, cleanser and toenail care  
 CC compositions, also in topical applications to damaged epithelial tissue  
 CC from sunburn, ulcers or puncture wounds so as to relieve pain, burning or  
 CC itching. The compositions can further be used to treat Crohn's disease,  
 CC skin grafts or diabetic ulcers. This peptide sequence, derived from human  
 CC hair or sheep wool keratin proteins, is a biologically active keratin  
 CC peptide of the invention.  
 XX Sequence 35 AA;  
 SQ Query Match 18.4%; Score 43; DB 7; Length 35;  
 Best Local Similarity 35.3%; Pred. No. 1.6e+02;  
 Matches 12; Conservative 4; Mismatches 8; Indels 10; Gaps 1;  
 QY 2 TLRCQ-----GPPGVLDLYRLEKLSRRYQ 25  
 ||||| | ||| : : : :  
 Db 2 TLRCQLGRLNVEVDAAPTVDLNRVLNSTRSQYE 35  
 RESULT 19  
 ADF22925  
 ID ADF22925 standard; peptide; 36 AA.  
 XX ADF22925;  
 XX 12-FEB-2004 (first entry)  
 DT Bioactive keratin peptide (SeqID 6055).  
 DE keratin; dermal fibroblast; epithelial tissue; cytokine-like activity;  
 KW antiinflammatory; antiulcer; vulnerary; analgesic;  
 KW cell proliferation activator; deodourant; cleanser; toenail care;  
 KW sunburn; puncture wound; Crohn's disease; skin graft; diabetic ulcer.  
 XX Unidentified.  
 OS WO2003064449-A2.  
 PN 07-AUG-2003.  
 PD 28-JAN-2003; 2003WO-US002645.  
 XX 28-JAN-2002; 2002US-0352396P.  
 PF (KERA-) KERAPLAST TECHNOLOGIES INC.  
 XX Cowsar DR;  
 PI WPI; 2003-812322/76.  
 DR Composition comprising an isolated bioactive keratin peptides useful for  
 PT cosmetic preparation, and treating conditions involving damaged, aged and  
 PT diseased epithelial tissue and skin.  
 XX Disclosure; SEQ ID NO 5895; 158pp; English.  
 PS This invention relates to a novel composition comprising an isolated  
 CC bioactive keratin peptide of 4-39 amino acids in length. Specifically, it  
 CC refers to keratin proteins that can stimulate the growth of dermal  
 CC fibroblasts for use in treating damaged, aged or diseased epithelial  
 CC tissue and skin. Furthermore, they exhibit cytokine-like activity,  
 CC particularly cell differentiation, adhesion and migration, and in  
 CC combination with other growth factors can be used to enhance the healing  
 CC activity of damaged skin or bone tissue. The present invention describes  
 CC these peptides as antiinflammatory, antiulcer, vulnerary, analgesic and  
 CC cell proliferation activators. Accordingly, there are various  
 CC applications for cosmetics e.g. deodourant, cleanser and toenail care  
 CC compositions, also in topical applications to damaged epithelial tissue  
 CC from sunburn, ulcers or puncture wounds so as to relieve pain, burning or  
 CC itching. The compositions can further be used to treat Crohn's disease,  
 CC skin grafts or diabetic ulcers. This peptide sequence, derived from human  
 CC hair or sheep wool keratin proteins, is a biologically active keratin  
 CC peptide of the invention.  
 XX Sequence 35 AA;  
 SQ Query Match 18.4%; Score 43; DB 7; Length 35;  
 Best Local Similarity 35.3%; Pred. No. 1.6e+02;  
 Matches 12; Conservative 4; Mismatches 8; Indels 10; Gaps 1;



XX (KERA-) KERAPLAST TECHNOLOGIES INC.  
 XX Cowsar DR;  
 XX WPI; 2003-812322/76.  
 XX Composition comprising an isolated bioactive keratin peptides useful for  
 XX cosmetic preparation, and treating conditions involving damaged, aged and  
 XX diseased epithelial tissue and skin.  
 XX Disclosure; SEQ ID NO 6055; 158pp; English.  
 XX This invention relates to a novel composition comprising an isolated  
 XX bioactive keratin peptide of 4-39 amino acids in length. Specifically, it  
 XX refers to keratin proteins that can stimulate the growth of dermal  
 XX fibroblasts for use in treating damaged, aged or diseased epithelial  
 XX tissue and skin. Furthermore, they exhibit cytokine-like activity,  
 XX particularly cell differentiation, adhesion and migration, and in  
 XX combination with other growth factors can be used to enhance the healing  
 XX activity of damaged skin or bone tissue. The present invention describes  
 XX these peptides as antiinflammatory, antiulcer, vulnerary, analgesic and  
 XX cell proliferation activators. Accordingly, there are various  
 XX applications for cosmetics e.g. deodorant, cleanser and toenail care  
 XX compositions, also in topical applications to damaged epithelial tissue  
 XX from sunburn, ulcers or puncture wounds so as to relieve pain, burning or  
 XX itching. The compositions can further be used to treat Crohn's disease,  
 XX skin grafts or diabetic ulcers. This peptide sequence, derived from human  
 XX hair or sheep wool keratin proteins, is a biologically active keratin  
 XX peptide of the invention.  
 XX Sequence 36 AA;  
 SQ Query Match 18.4%; Score 43; DB 7; Length 36;  
 Best Local Similarity 35.3%; Pred. No. 1.7e+02;  
 Matches 12; Conservative 4; Mismatches 8; Indels 10; Gaps 1;  
 QY 2 TLRCQ-----GPPGVLDYRLEKLSRSRYQ 25  
 ||||| : : : : :  
 Db 2 TLRCQLGDRNLNVEVDAAPTVDLNRVLNETRSQYE 35  
 ||||| : : : : :  
 RESULT 20  
 ADF22957  
 ID ADF22957 standard; peptide; 36 AA.  
 XX ADF22957;  
 AC ADF22957;  
 XX 12-FEB-2004 (first entry)  
 DT Bioactive keratin peptide (SeqID 6087).  
 DE keratin; dermal fibroblast; epithelial tissue; cytokine-like activity;  
 KW antiinflammatory; antiulcer; vulnerary; analgesic;  
 KW cell proliferation activator; deodorant; cleanser; toenail care;  
 KW sunburn; puncture wound; Crohn's disease; skin graft; diabetic ulcer.  
 XX Unidentified.  
 OS WO2003064449-A2.  
 XX 07-AUG-2003.  
 PD 28-JAN-2003; 2003WO-US002645.  
 PF 28-JAN-2002; 2002US-0352396P.  
 XX (KERA-) KERAPLAST TECHNOLOGIES INC.  
 XX Cowsar DR;  
 XX WPI; 2003-812322/76.  
 XX Composition comprising an isolated bioactive keratin peptides useful for  
 XX cosmetic preparation, and treating conditions involving damaged, aged and  
 XX diseased epithelial tissue and skin.  
 XX Disclosure; SEQ ID NO 6023; 158pp; English.  
 XX This invention relates to a novel composition comprising an isolated

PT Composition comprising an isolated bioactive keratin peptides useful for  
 PT cosmetic preparation, and treating conditions involving damaged, aged and  
 PT diseased epithelial tissue and skin.  
 XX Disclosure; SEQ ID NO 6087; 158pp; English.  
 XX This invention relates to a novel composition comprising an isolated  
 XX bioactive keratin peptide of 4-39 amino acids in length. Specifically, it  
 XX refers to keratin proteins that can stimulate the growth of dermal  
 XX fibroblasts for use in treating damaged, aged or diseased epithelial  
 XX tissue and skin. Furthermore, they exhibit cytokine-like activity,  
 XX particularly cell differentiation, adhesion and migration, and in  
 XX combination with other growth factors can be used to enhance the healing  
 XX activity of damaged skin or bone tissue. The present invention describes  
 XX these peptides as antiinflammatory, antiulcer, vulnerary, analgesic and  
 XX cell proliferation activators. Accordingly, there are various  
 XX applications for cosmetics e.g. deodorant, cleanser and toenail care  
 XX compositions, also in topical applications to damaged epithelial tissue  
 XX from sunburn, ulcers or puncture wounds so as to relieve pain, burning or  
 XX itching. The compositions can further be used to treat Crohn's disease,  
 XX skin grafts or diabetic ulcers. This peptide sequence, derived from human  
 XX hair or sheep wool keratin proteins, is a biologically active keratin  
 XX peptide of the invention.  
 XX Sequence 36 AA;  
 SQ Query Match 18.4%; Score 43; DB 7; Length 36;  
 Best Local Similarity 35.3%; Pred. No. 1.7e+02;  
 Matches 12; Conservative 4; Mismatches 8; Indels 10; Gaps 1;  
 QY 2 TLRCQ-----GPPGVLDYRLEKLSRSRYQ 25  
 ||||| : : : : :  
 Db 1 TLRCQLGDRNLNVEVDAAPTVDLNRVLNETRSQYE 34  
 ||||| : : : : :  
 RESULT 21  
 ADF22893  
 ID ADF22893 standard; peptide; 36 AA.  
 XX ADF22893;  
 AC ADF22893;  
 XX 12-FEB-2004 (first entry)  
 DT Bioactive keratin peptide (SeqID 6023).  
 DE keratin; dermal fibroblast; epithelial tissue; cytokine-like activity;  
 KW antiinflammatory; antiulcer; vulnerary; analgesic;  
 KW cell proliferation activator; deodorant; cleanser; toenail care;  
 KW sunburn; puncture wound; Crohn's disease; skin graft; diabetic ulcer.  
 XX Unidentified.  
 OS WO2003064449-A2.  
 XX 07-AUG-2003.  
 PD 28-JAN-2003; 2003WO-US002645.  
 PF 28-JAN-2002; 2002US-0352396P.  
 XX (KERA-) KERAPLAST TECHNOLOGIES INC.  
 XX Cowsar DR;  
 XX WPI; 2003-812322/76.  
 XX Composition comprising an isolated bioactive keratin peptides useful for  
 XX cosmetic preparation, and treating conditions involving damaged, aged and  
 XX diseased epithelial tissue and skin.  
 XX Disclosure; SEQ ID NO 6023; 158pp; English.  
 XX This invention relates to a novel composition comprising an isolated

bioactive keratin peptide of 4-39 amino acids in length. Specifically, it refers to keratin proteins that can stimulate the growth of dermal fibroblasts for use in treating damaged, aged or diseased epithelial tissue and skin. Furthermore, they exhibit cytokine-like activity, particularly cell differentiation, adhesion and migration, and in combination with other growth factors can be used to enhance the healing activity of damaged skin or bone tissue. The present invention describes these peptides as antiinflammatory, antiulcer, vulnery, analgesic and cell proliferation activators. Accordingly, there are various applications for cosmetics e.g. deodorant, cleanser and tonal care compositions, also in topical applications to damaged epithelial tissue from sunburn, ulcers or puncture wounds so as to relieve pain, burning or itching. The compositions can further be used to treat Crohn's disease, skin grafts or diabetic ulcers. This peptide sequence, derived from human hair or sheep wool keratin proteins, is a biologically active keratin peptide of the invention.

Query Match	18.4%	Score 43;	DB 7;	Length 36;
Best Local Similarity	35.3%	Pred. No. 1.7e+02;		
Matches 12;	Conservative 4;	Mismatches 8;	Indels 10;	Gaps 1;

Qy	2 TLRCQ-----GPPGVDLVRLKLSRRYQ 25             :   : :
Db	3 TLRCLGDRLNVEVDAAPTVLNRVLNETRQYE 36

RESULT 22  
ADF23053  
ID ADF23053 standard; peptide; 37 AA.

XX	
XX	
AC	ADF23053;
XX	
XX	
DT	12-FEB-2004 (first entry)
XX	
XX	Bioactive keratin peptide (SeqID 6183) .
DE	
XX	keratin; dermal fibroblast; epithelial tissue; cytokine-like activity;
KW	antiinflammatory; antitumor; cutaneous; vulvular; analgesic;
KW	cell proliferation activator; deodorant; cleanser; toenail care;
KW	skin burn; puncture wound; Crohn's disease; skin graft; diabetic ulcer.

XX Composition comprising an isolated bioactive keratin peptides useful for  
PT cosmetic preparation, and treating conditions involving damaged, aged and  
PT diseased epithelial tissue and skin.  
XX  
XX Disclosure; SEQ ID NO 6183; 158pp. English.  
PS

This invention relates to a novel composition comprising an isolated bioactive keratin peptide of 4-39 amino acids in length. Specifically, it refers to keratin proteins that can stimulate the growth of dermal fibroblasts for use in treating damaged, aged or diseased epithelial tissue and skin. Furthermore, they exhibit cytokine-like activity, particularly cell differentiation, adhesion and migration, and in combination with other growth factors can be used to enhance the healing activity of damaged skin or bone tissue. The present invention describes

these peptides as antinflammatory, antiulcer, vulnerary, analgesic and cell proliferation activators. Accordingly, there are various applications for cosmetics e.g. deodorant, cleanser and tonal care compositions, also in topical applications to damaged epithelial tissue from sunburn, ulcers or puncture wounds so as to relieve pain, burning or itching. The compositions can further be used to treat Crohn's disease, skin grafts or diabetic ulcers. This peptide sequence, derived from human hair or sheep wool keratin proteins, is a biologically active keratin peptide of the invention.

Query Match 18.4%; Score 43; DB 7; Length 37;  
Best Local Similarity 35.3%; Pred. NO. 1.7e+02;  
Matches 12; Conservative 4; Mismatches 8; Indels

Qy 2 TLRCQ-----GPPGVLYRLEKLSRRYQ 25  
||||| | ||| : : :  
D'b 2 TLRCQGLRLNVEVDAAPTVLNRLNTRSQYE 35

RESULT 23  
ADF22989  
ID ADF22989 standard; peptide: 37 AA.

XX	
XX	
AC	
XX	
ADP22989;	
XX	
DT	12-FEB-2004 (first entry)
XX	
DE	Bioactive keratin peptide (SeqID 6119) .
XX	
KW	keratin; dermal fibroblast; epithelial tissue; cytokine-like activity;
KW	antiinflammatory; antitumor; vulnerrary; analgesic;
KW	cell proliferation activator; deodorant; cleanser; toenail care;
KW	sunburn; puncture wound; Crohn's disease; skin graft; diabetic ulcer.

Composition comprising an isolated bioactive keratin peptides useful for cosmetic preparation, and treating conditions involving damaged, aged and diseased epithelial tissue and skin.

PS Disclosure; SEQ ID NO 6119; 158pp; English.

This invention relates to a novel composition comprising an isolated bioactive keratin peptide of 4-39 amino acids in length. Specifically, it refers to keratin proteins that can stimulate the growth of dermal fibroblasts for use in treating damaged, aged or diseased epithelial tissue and skin. Furthermore, they exhibit cytokine-like activity, particularly cell differentiation, adhesion and migration, and in combination with other growth factors can be used to enhance the healing activity of damaged skin or bone tissue. The present invention describes these peptides as antiinflammatory, antiulcer, vinylicary, analgesic and cell proliferation activators. Accordingly, there are various applications for cosmetics e.g. deodorant, cleanser and toenail care compositions, also in topical applications to damaged epithelial tissue from sunburn, ulcers or puncture wounds so as to relieve pain, burning or itching. The compositions can further be used to treat Crohn's disease, skin grafts or diabetic ulcers. This peptide sequence, derived from human

CC hair or sheep wool keratin proteins, is a biologically active keratin  
XX peptide of the invention.

SQ Sequence 37 AA;

Query Match 18.4%; Score 43; DB 7; Length 37;  
Best Local Similarity 35.3%; Pred. No. 1.7e+02;  
Matches 12; Conservative 4; Mismatches 8; Indels 10; Gaps 1;

QY 2 TLRCQ-----GPGVDLYRLEKLSRRYQ 25  
||||| : : : : :  
DB 4 TLRCQLGDLNVEVDAAPTVDLNRVNETRSQYE 37

RESULT 24

ID ADF23021  
ID ADF23021 standard; peptide; 37 AA.

XX ADF23021;

XX 12-FEB-2004 (first entry)

XX Bioactive keratin peptide (SeqID 6151).

XX keratin; dermal fibroblast; epithelial tissue; cytokine-like activity;  
KW antiinflammatory; antiulcer; vulnerary; analgesic;  
KW cell proliferation activator; deodorant; cleanser; toenail care;  
KW sunburn; puncture wound; Crohn's disease; skin graft; diabetic ulcer.

XX Unidentified.

XX WO2003064449-A2.

XX 07-AUG-2003.

XX 28-JAN-2003; 2003WO-US002645.

XX 28-JAN-2002; 2002US-0352396P.

XX (KERA-) KERAPLAST TECHNOLOGIES INC.

XX Cowsar DR;

XX WPI; 2003-812322/76.

XX Composition comprising an isolated bioactive keratin peptides useful for  
PT cosmetic preparation, and treating conditions involving damaged, aged and  
PT diseased epithelial tissue and skin.

XX Disclosure; SEQ ID NO 6151; 159pp; English.

XX This invention relates to a novel composition comprising an isolated  
CC bioactive keratin peptide of 4-39 amino acids in length. Specifically, it  
CC refers to keratin proteins that can stimulate the growth of dermal  
CC fibroblasts for use in treating damaged, aged or diseased epithelial  
CC tissue and skin. Furthermore, they exhibit cytokine-like activity,  
CC particularly cell differentiation, adhesion and migration, and in  
CC combination with other growth factors can be used to enhance the healing  
CC activity of damaged skin or bone tissue. The present invention describes  
CC these peptides as antiinflammatory, antiulcer, vulnerary, analgesic and  
CC cell proliferation activators. Accordingly, there are various  
CC applications for cosmetics e.g. deodorant, cleanser and toenail care  
CC compositions, also in topical applications to damaged epithelial tissue  
CC from sunburn, ulcers or puncture wounds so as to relieve pain, burning or  
CC itching. The compositions can further be used to treat Crohn's disease,  
CC skin grafts or diabetic ulcers. This peptide sequence, derived from human  
CC hair or sheep wool keratin proteins, is a biologically active keratin  
CC peptide of the invention.

XX Sequence 37 AA;

Query Match 18.4%; Score 43; DB 7; Length 37;  
Best Local Similarity 35.3%; Pred. No. 1.7e+02;

Matches 12; Conservative 4; Mismatches 8; Indels 10; Gaps 1;

QY 2 TLRCQ-----GPGVDLYRLEKLSRRYQ 25  
||||| : : : : :  
DB 3 TLRCQLGDLNVEVDAAPTVDLNRVNETRSQYE 36

RESULT 25

ID ADF23117  
ID ADF23117 standard; peptide; 38 AA.

XX ADF23117;

XX 12-FEB-2004 (first entry)

XX Bioactive keratin peptide (SeqID 6247).

XX keratin; dermal fibroblast; epithelial tissue; cytokine-like activity;  
KW antiinflammatory; antiulcer; vulnerary; analgesic;  
KW cell proliferation activator; deodorant; cleanser; toenail care;  
KW sunburn; puncture wound; Crohn's disease; skin graft; diabetic ulcer.

XX Unidentified.

XX WO2003064449-A2.

XX 07-AUG-2003.

XX 28-JAN-2003; 2003WO-US002645.

XX 28-JAN-2002; 2002US-0352396P.

XX (KERA-) KERAPLAST TECHNOLOGIES INC.

XX Cowsar DR;

XX WPI; 2003-812322/76.

XX Composition comprising an isolated bioactive keratin peptides useful for  
PT cosmetic preparation, and treating conditions involving damaged, aged and  
PT diseased epithelial tissue and skin.

XX Disclosure; SEQ ID NO 6247; 159pp; English.

XX This invention relates to a novel composition comprising an isolated  
CC bioactive keratin peptide of 4-39 amino acids in length. Specifically, it  
CC refers to keratin proteins that can stimulate the growth of dermal  
CC fibroblasts for use in treating damaged, aged or diseased epithelial  
CC tissue and skin. Furthermore, they exhibit cytokine-like activity,  
CC particularly cell differentiation, adhesion and migration, and in  
CC combination with other growth factors can be used to enhance the healing  
CC activity of damaged skin or bone tissue. The present invention describes  
CC these peptides as antiinflammatory, antiulcer, vulnerary, analgesic and  
CC cell proliferation activators. Accordingly, there are various  
CC applications for cosmetics e.g. deodorant, cleanser and toenail care  
CC compositions, also in topical applications to damaged epithelial tissue  
CC from sunburn, ulcers or puncture wounds so as to relieve pain, burning or  
CC itching. The compositions can further be used to treat Crohn's disease,  
CC skin grafts or diabetic ulcers. This peptide sequence, derived from human  
CC hair or sheep wool keratin proteins, is a biologically active keratin  
CC peptide of the invention.

XX Sequence 38 AA;

Query Match 18.4%; Score 43; DB 7; Length 38;  
Best Local Similarity 35.3%; Pred. No. 1.8e+02;  
Matches 12; Conservative 4; Mismatches 8; Indels 10; Gaps 1;

QY 2 TLRCQ-----GPGVDLYRLEKLSRRYQ 25  
||||| : : : : :  
DB 3 TLRCQLGDLNVEVDAAPTVDLNRVNETRSQYE 36

Search completed: October 31, 2005, 17:58:53  
Job time : 166 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 31, 2005, 17:55:59 ; Search time 42 Seconds  
(without alignments)  
79.981 Million cell updates

Title: US-09-503-387-3\_COPY 44 88

Perfect score: 234

Sequence: 1 VTLRCQGPVGVDLYRLEKLS.....DQAVLFIPAMKRSLAGRYRC 45

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 268441

Minimum DB seq length: 0

Maximum DB seq length:	0
Maximum DB seq length:	46

Post-processing: Minimum Match 0%

Loss processing: Minimum Match 0%  
Maximum Match 100%

**Listing first 100 summaries**

Database : Issued Patents AA:\*

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2: /cgn2\_6/prodata/1/iaa/5B\_COMB.pcp.\*

3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*

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4: /cgn2_6/ptodata/1/1aa/6B_COMB.per:*
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5: /cgn2_6/ptodata/1/1aa/PCTUS COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backf11aa1 non.*
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b: /cgnz\_b/ptodata/1/1aa/back111est.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	216	92.3	41	3	US-09-345-468-6	Sequence 6, Appli
2	216	92.3	41	3	US-09-414-458A-6	Sequence 6, Appli
3	164	70.1	41	3	US-09-345-468-22	Sequence 22, Appl
4	164	70.1	41	3	US-09-414-453A-22	Sequence 22, Appl
5	39	16.7	36	3	US-08-554-385-23	Sequence 23, Appl
6	38	16.2	42	2	US-08-429-764A-3	Sequence 3, Appli
7	37.5	16.0	35	3	US-09-461-697-33	Sequence 393, App
8	36.5	15.6	33	1	US-07-662-007B-30	Sequence 30, Appl
9	36.5	15.6	23	1	US-07-824-247-30	Sequence 30, Appl
10	36.5	15.6	23	3	US-08-470-204A-30	Sequence 30, Appl
11	36	15.4	32	4	US-08-840-713-40	Sequence 40, Appl
12	36	15.4	35	4	US-10-038-613-54	Sequence 54, Appl
13	36	15.4	44	4	US-09-865-621A-16	Sequence 16, Appl
14	36	15.4	46	4	US-09-865-621A-11	Sequence 11, Appl
15	35.5	15.2	37	1	US-07-977-630-58	Sequence 58, Appl
16	35	15.0	22	1	US-07-934-656A-17	Sequence 17, Appl
17	35	15.0	22	1	US-07-934-656A-18	Sequence 18, Appl
18	35	15.0	30	4	US-09-828-645-7	Sequence 7, Appli
19	35	15.0	32	4	US-09-647-468-117	Sequence 117, App
20	35	15.0	35	4	US-10-038-612-53	Sequence 53, Appl
21	35	15.0	45	4	US-09-574-377-30	Sequence 30, Appl
22	34.5	14.7	45	2	US-08-332-562A-22	Sequence 22, Appl
23	34	14.5	20	2	US-08-480-190-180	Sequence 180, App
24	34	14.5	20	2	US-08-488-379-180	Sequence 180, App
25	34	14.5	20	4	US-08-475-399A-180	Sequence 180, App
26	34	14.5	20	4	US-08-077-255A-180	Sequence 180, App
27	34	14.5	20	5	PCT-US93-075545-180	Sequence 180, App



COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM PS/2 Model 502 or 55SX  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/554,385  
FILING DATE: No. 6017692ember 8, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Karen F. Lech  
REGISTRATION NUMBER: 35,238  
REFERENCE/DOCKET NUMBER: 00786/252001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-554-385-23

Query Match 16.7%; Score 39; DB 3; Length 36;  
Best Local Similarity 52.6%; Pred. No. 1e+02;  
Matches 10; Conservative 3; Mismatches 4; Indels 4; Gaps 1;

QY 3 LRCQGGPPGVLDYRLKLSL 21  
DB 10 LRLVTPGAEL--LKKISS 26

## RESULT 6

US-08-429-764A-3  
Sequence 3, Application US/08429764A  
Patent No. 5830647

GENERAL INFORMATION:  
APPLICANT: Eaton, Dan L.  
APPLICANT: de Sauvage, Frederic J.  
TITLE OF INVENTION: MPL LIGAND  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/429,764A  
FILING DATE: 26-Apr-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/348658  
FILING DATE: 02-DEC-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/185607  
FILING DATE: 21-JAN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/176553  
FILING DATE: 03-JAN-1994  
ATTORNEY/AGENT INFORMATION:

NAME: Winter, Daryl B.  
REGISTRATION NUMBER: 32,637  
REFERENCE/DOCKET NUMBER: P0871P1C1D4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1249  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 42 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-429-764A-3

Query Match 16.2%; Score 38; DB 2; Length 42;  
Best Local Similarity 47.4%; Pred. No. 1.8e+02;  
Matches 9; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 VTLRCQGGPPGVLDYRLKSL 19  
DB 13 LTLSSPAPPACDLRLVLSKL 31

## RESULT 7

US-09-461-697-393  
Sequence 393, Application US/09461697  
Patent No. 6277974

GENERAL INFORMATION:  
APPLICANT: COGENT NEUROSCIENCE, Inc.  
APPLICANT: Lo, Donald C.  
APPLICANT: Barney, Shawn  
APPLICANT: Thomas, Mary Beth  
APPLICANT: Portbury, Stuart D.  
APPLICANT: Puranam, Kasturi  
APPLICANT: Katz, Lawrence C.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING  
TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING  
FILE REFERENCE: 10001-005-999  
CURRENT APPLICATION NUMBER: US/09/461,697  
CURRENT FILING DATE: 1999-12-14  
NUMBER OF SEQ ID NOS: 466  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 393  
LENGTH: 35  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-461-697-393

Query Match 16.0%; Score 37.5; DB 3; Length 35;  
Best Local Similarity 47.4%; Pred. No. 1.7e+02;  
Matches 9; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

QY 26 DQAV-LFIPAMKRSLAGRY 43  
DB 14 DQAAGVFCPLFRSRSGHY 32

## RESULT 8

US-07-682-007B-30  
Sequence 30, Application US/07662007B  
Patent No. 5344771

GENERAL INFORMATION:  
APPLICANT: Davies, Huw Maelor  
APPLICANT: Pollard, Michael Roman  
APPLICANT: Voekler, Toni Alois  
APPLICANT: Thompson, Gregory A.  
TITLE OF INVENTION: Plant Thioesterases  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Calgene, Inc.  
STREET: 1920 Fifth Street  
CITY: Davis

```
; STATE: California
; COUNTRY: USA
; ZIP: 95616
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 KB storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.7
; SOFTWARE: MicrosoftWord 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/662,007B
; FILING DATE: 19910408
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/514,030
; FILING DATE: 26-APR-1990
; APPLICATION NUMBER: 07/620,426
; FILING DATE: 30-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth Lassen
; REGISTRATION NUMBER: 31,845
; REFERENCE/DOCKET NUMBER: CGNE 70-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 916-753-6313
; TELEFAX: 916-753-1510
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-662-007B-30

Query Match 15.6%; Score 36.5; DB 1; Length 23;
Best Local Similarity 36.4%; Pred. No. 1.4e+02;
Matches 8; Conservative 7; Mismatches 6; Indels 1; Gaps 1;

Qy 12 DLYRLEKLSRRYQDQAVLFIP 33
| |||::: :|: |||
Db 3 DTRRLQKVND-VEDEVLFVFP 23

RESULT 9
US-07-824-247-30
; Sequence 30, Application US/07824247
; Patent No. 5512482
; GENERAL INFORMATION:
; APPLICANT: Voelker, Toni Alois
; TITLE OF INVENTION: Plant Thioesterases
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calgene, Inc.
; STREET: 1920 Fifth Street
; CITY: Davis
; STATE: California
; COUNTRY: USA
; ZIP: 95616
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 KB storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.7
; SOFTWARE: MicrosoftWord 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/824,247
; FILING DATE: 19920122
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/782,263
; FILING DATE: 24-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/773,096
; FILING DATE: 7-OCT-1991
; APPLICATION NUMBER: 07/704,861
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; FILING DATE: 21-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/02960
; FILING DATE: 25-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/662,007
; FILING DATE: 27-FEB-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/620,426
; FILING DATE: 30-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/514,030
; FILING DATE: 26-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth Lassen
; REGISTRATION NUMBER: 31,845
; NAME: Donna E. Scherer
; REGISTRATION NUMBER: 34,719
; REFERENCE/DOCKET NUMBER: CGNE 82-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 916-753-6313
; TELEFAX: 916-753-1510
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-824-247-30

Query Match 15.6%; Score 36.5; DB 1; Length 23;
Best Local Similarity 36.4%; Pred. No. 1.4e+02;
Matches 8; Conservative 7; Mismatches 6; Indels 1; Gaps 1;

Qy 12 DLYRLEKLSRRYQDQAVLFIP 33
| |||::: :|: |||
Db 3 DTRRLQKVND-VEDEVLFVFP 23

RESULT 10
US-08-470-204A-30
; Sequence 30, Application US/08470204A
; Patent No. 6028247
; GENERAL INFORMATION:
; APPLICANT: Voelker, Toni Alois
; TITLE OF INVENTION: Plant Thioesterases
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calgene, Inc.
; STREET: 1920 Fifth Street
; CITY: Davis
; STATE: California
; COUNTRY: USA
; ZIP: 95616
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB
; COMPUTER: Apple Macintosh IICI
; OPERATING SYSTEM: Macintosh 7.1
; SOFTWARE: MicrosoftWord 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,204A
; FILING DATE: 06-JUN-95
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/824,247
; FILING DATE: 22-JAN-1992
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/782,263
; FILING DATE: 24-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/773,096
; FILING DATE: 7-OCT-1991
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PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/704,861  
; FILING DATE: 21-MAY-1991  
PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US91/02960  
; FILING DATE: 25-APR-1991  
PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/662,007  
; FILING DATE: 27-FEB-1991  
PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/620,426  
; FILING DATE: 30-NOV-1990  
PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/514,030  
; FILING DATE: 26-APR-1990  
ATTORNEY/AGENT INFORMATION:  
; NAME: Elizabeth Lassen  
; REGISTRATION NUMBER: 31,845  
; NAME: Donna E. Scherer  
; REGISTRATION NUMBER: 34,719  
; REFERENCE/DOCKET NUMBER: CGNE 82-3  
TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 916-753-6313  
; TELEFAX: 916-753-1510  
INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 23 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-470-204A-30

Query Match 15.6%; Score 36.5; DB 3; Length 23;  
Best Local Similarity 36.4%; Pred. No. 1.4e+02;  
Matches 8; Conservative 7; Mismatches 6; Indels 1; Gaps 1;

OY 12 DLYRLEKLSRRYQQAVLFIP 33  
| | | | | : : : : :  
Db 3 DTRRLQKVND-VEDEYLVFIP 23

RESULT 11  
US-08-840-713-40  
; Sequence 40, Application US/08840713  
; Patent No. 6498233  
GENERAL INFORMATION:  
; APPLICANT: WELS, Winfried, Dr.  
; APPLICANT: FOYMINAYA, Jesus  
; TITLE OF INVENTION: NUCLEIC ACID TRANSFER SYSTEM  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nikaide, Marmelstein, Murray & Oram LLP  
; STREET: 655 15th St., N.W., Suite 330 - G St. Lobby  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-5701  
COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/840,713  
; FILING DATE: 25-APR-1997  
; CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
; NAME: Kitts, Monica Chin  
; REGISTRATION NUMBER: 36,105  
; REFERENCE/DOCKET NUMBER: 1614-7014  
TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 638 - 5000  
; TELEFAX: (202) 638 - 4810

INFORMATION FOR SEQ ID NO: 40:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-840-713-40

Query Match 15.4%; Score 36; DB 4; Length 12;  
Best Local Similarity 63.6%; Pred. No. 75;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 17 EKLSSRYQDQ 27  
| | | | | : : : : :  
Db 1 EKLESSDYKDE 11

RESULT 12  
US-10-038-612-54  
; Sequence 54, Application US/10038612  
; Patent No. 6723830  
GENERAL INFORMATION:  
; APPLICANT: Ben-Sasson, Shmuel A.  
; TITLE OF INVENTION: Short Peptides Which Selectively  
; FILE REFERENCE: 1242.1029-000 (CMCC-679)  
; CURRENT APPLICATION NUMBER: US/10/038,612  
; CURRENT FILING DATE: 2002-01-08  
; PRIOR APPLICATION NUMBER: US 09/161,094  
; PRIOR FILING DATE: 1998-09-25  
; NUMBER OF SEQ ID NOS: 172  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 54  
; LENGTH: 35  
; TYPE: PPT  
; ORGANISM: unknown  
; FEATURE:  
; OTHER INFORMATION: FGFR-4  
US-10-038-612-54

Query Match 15.4%; Score 36; DB 4; Length 35;  
Best Local Similarity 63.6%; Pred. No. 2.8e+02;  
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 3 LRCQPGPGVDL 13  
| | | | | : : : : :  
Db 13 LRARRPGPDL 23

RESULT 13  
US-09-865-621A-16  
; Sequence 16, Application US/09865621A  
; Patent No. 6555348  
GENERAL INFORMATION:  
; APPLICANT: JORGENSEN, FLEMMING  
; APPLICANT: HANSEN, OLE CAI  
; APPLICANT: STOUGAARD, PETER  
; TITLE OF INVENTION: A NEW ENZYME ISOLATED FROM A BIFIDOBACTERIUM  
; FILE REFERENCE: 02405.0200  
; CURRENT APPLICATION NUMBER: US/09/865,621A  
; CURRENT FILING DATE: 2001-05-29  
; PRIOR APPLICATION NUMBER: 60/207,154  
; PRIOR FILING DATE: 2000-05-26  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 16  
; LENGTH: 44  
; TYPE: PPT  
; ORGANISM: Escherichia coli  
US-09-865-621A-16

Query Match 15.4%; Score 36; DB 4; Length 44;  
Best Local Similarity 23.3%; Pred. No. 3.8e+02;

Matches 10; Conservative 9; Mismatches 16; Indels 8; Gaps 2;  
Qy 5 CQPPGVDLVR-----LEKLSRRYQDQVLFIFAMKRSLAGR 42  
Db 3 CYTSP---IYREKTAIIDRLAERYKDHAPALILWHISNEFEQ 42

RESULT 14  
US-09-865-621A-11  
; Sequence 11, Application US/09865621A  
; Patent No. 655348  
; GENERAL INFORMATION:  
; APPLICANT: JORGENSEN, FLEMING  
; APPLICANT: HANSEN, OLE CAJ  
; APPLICANT: STOUGAARD, PETER  
; TITLE OF INVENTION: A NEW ENZYME ISOLATED FROM A BIFIDOBACTERIUM  
; FILE REFERENCE: 02405.0200  
; CURRENT APPLICATION NUMBER: US/09/865.621A  
; CURRENT FILING DATE: 2001-05-29  
; PRIOR APPLICATION NUMBER: 60/207,154  
; PRIOR FILING DATE: 2000-05-26  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 46  
; TYPE: PRT  
; ORGANISM: Escherichia coli  
US-09-865-621A-11

Query Match 15.4%; Score 36; DB 4; Length 46;  
Best Local Similarity 34.6%; Pred. No. 4e+02;  
Matches 9; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

Qy 19 LSSRYQDQVLFIFAMKRSLAGRYR 44  
Db 2 ISSAWYYSVQYAAKMTALARYK 27

RESULT 15  
US-07-977-630-58  
; Sequence 58, Application US/07977630  
; Patent No. 5583038  
; GENERAL INFORMATION:  
; APPLICANT: Stover, Charles K.  
; TITLE OF INVENTION: BACTERIAL EXPRESSION VECTORS CONTAINING  
; TITLE OF INVENTION: DNA ENCODING SECRETION SIGNALS OF LIPOPROTEINS  
; NUMBER OF SEQUENCES: 84  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,  
; ADDRESSEE: Stewart & Olstein  
; STREET: 6 Becker Farm Road  
; CITY: Roseland  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07068  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch diskette  
; COMPUTER: IBM  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/977.630  
; FILING DATE: No. 5583038ember 17, 1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Herion, Charles J.  
; REGISTRATION NUMBER: 28,019  
; REFERENCE/DOCKET NUMBER: 459201-174  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-994-1700  
; TELEFAX: 201-994-1744  
; INFORMATION FOR SEQ ID NO: 58:  
; SEQUENCE CHARACTERISTICS:

; LENGTH: 37 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-07-977-630-58

Query Match 15.2%; Score 35.5; DB 1; Length 37;  
Best Local Similarity 30.6%; Pred. No. 3.6e+02;  
Matches 11; Conservative 6; Mismatches 14; Indels 5; Gaps 1;  
Qy 14 YRLEKLSRRYQDQ-----AVLFIPAMKRSLAGRYR 44  
Db 1 HELRSLARLYRNQIGDKFACRLLGHKSDSMAARYR 36

RESULT 16  
US-07-934-656A-17  
; Sequence 17, Application US/07934656A  
; Patent No. 5500347  
; GENERAL INFORMATION:  
; APPLICANT: MOLL, Roland  
; APPLICANT: FRANK, Werner W.  
; TITLE OF INVENTION: PROCESS FOR THE PURIFICATION OF  
; TITLE OF INVENTION: CYTOKERATIN 20 AND ITS USE FOR THE PRODUCTION OF  
; TITLE OF INVENTION: ANTIBODIES  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram  
; STREET: 655 Fifteenth Street N.W. Suite 330  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005-5701  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/934.656A  
; FILING DATE: 27-JAN-1993  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE P 40 23 945.4  
; FILING DATE: 27-JUL-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Murray, Robert B.  
; REGISTRATION NUMBER: 22,980  
; REFERENCE/DOCKET NUMBER: P364-3003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)638-5000  
; TELEFAX: (202)638-4810  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 22 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-07-934-656A-17

Query Match 15.0%; Score 35; DB 1; Length 27;  
Best Local Similarity 43.8%; Pred. No. 2.2e+02;  
Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 1 VTLRCQGPVGVLYRL 16  
Db 1 VNVEMDAAPGVDSRI 16

RESULT 17  
US-07-934-656A-18  
; Sequence 18, Application US/07934656A  
; Patent No. 5500347

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; GENERAL INFORMATION:
; APPLICANT: MOLL, Roland
; APPLICANT: FRANK, Werner W.
; TITLE OF INVENTION: PROCESS FOR THE PURIFICATION OF
; TITLE OF INVENTION: CYTOKERATIN 20 AND ITS USE FOR THE PRODUCTION OF
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram
; STREET: 655 Fifteenth Street N.W. Suite 330
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,656A
; FILING DATE: 27-JAN-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 40 23 945.4
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Murray, Robert B.
; REGISTRATION NUMBER: 22,980
; REFERENCE/DOCKET NUMBER: P564-3003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-5000
; TELEFAX: (202)638-4810
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-934-656A-18

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```

Query Match      15.0%; Score 35; DB 1; Length 22;
Best Local Similarity 43.8%; Pred. No. 2.2e+02;
Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 1 VTLRCQGGPPGVDLTRL 16
    | | | | | | |
Db 1 NVVEMDAAPGVDLTRL 16

```

```

RESULT 18
US-09-828-645-7
; Sequence 7, Application US/09828645
; Patent No. 6743593
; GENERAL INFORMATION:
; APPLICANT: Hu, Yao Xiong
; TITLE OF INVENTION: Immunological Methodology for Discerning Human Papillomavirus
; FILE REFERENCE: 146-1-002
; CURRENT APPLICATION NUMBER: US/09/828,645
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US 60/194,796
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Derived from the E7 early region of HPV-16
; NAME/KEY: misc_feature
; LOCATION: (19)..(19)
; OTHER INFORMATION: Xaa = L-carboxymethylcysteine

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```

US-09-828-645-7

Query Match      15.0%; Score 35; DB 4; Length 30;
Best Local Similarity 36.8%; Pred. No. 3.3e+02;
Matches 7; Conservative 4; Mismatches 8; Indels 0; Gaps 0

Qy      8 PPGVDLYRLEKLSRRYQD 26
      |  |||  ||:|  |  :
Db      12 PETTDLYRQLNDSSEE 30

RESULT 19
US-09-647-468-117
; Sequence 117, Application US/09647468
; Patent No. 6677436
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; APPLICANT: YABUTA, NAOMIRO
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
; FILE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
; FILE REFERENCE: 053466/0289
; CURRENT APPLICATION NUMBER: US/09/647,468
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 117
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence
; OTHER INFORMATION: of PR3 of versions "d1" and "d3" of humanized H
; OTHER INFORMATION: chain V region
; US-09-647-468-117

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```

Query Match      15.0%; Score 35; DB 4; Length 32;
Best Local Similarity 57.1%; Pred. No. 3.6e+02;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY      18  KLSRRYQDQAVLF 31
Db       16  ELSSLRSEDSAVYF 29

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RESULT 20
US-10-038-612-53
; Sequence 53, Application US/10038612
; Patent No. 6723830
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson, Shmuel A.
; TITLE OF INVENTION: Short Peptides Which Selectively
; Modulate the Activity of Protein Kinases
; FILE REFERENCE: 1242.1029-000 (CMCC-679)
; CURRENT APPLICATION NUMBER: US/10/038.612
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 09/161,094
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 35
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: FGFR-3
US-10-038-612-53
Query Match 15.0%; Score 35; DB 4; Length 35;

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STRANDEDNESS:  
TOPOLOGY: linear  
US-08-480-190-180

Query Match 14.5%; Score 34; DB 2; Length 20;  
Best Local Similarity 50.0%; Pred. No. 2.8e+02;  
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 7 GPPGVDLYRLEK 18  
|||:|:|  
Db 1 GPPKLDIRKEEK 12

## RESULT 24

US-08-488-379-180  
; Sequence 180, Application US/08488379  
; Patent No. 5880103  
; GENERAL INFORMATION:  
; APPLICANT: Robert G. Urban  
; APPLICANT: Roman M. Chicz  
; APPLICANT: Dario A. A. Vignali  
; APPLICANT: Mary L. Hedley  
; APPLICANT: Lawrence J. Stern  
; APPLICANT: Jack L. Strominger  
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
; NUMBER OF SEQUENCES: 274  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; COMPUTER: IBM PS/2 Model 50Z or 55SX  
; OPERATING SYSTEM: MS-DOS (Version 5.0)  
; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/488,379  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/077,255  
; FILING DATE: June 15, 1993  
; APPLICATION NUMBER: 07/925,460  
; FILING DATE: August 11, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clark, Paul T.  
; REGISTRATION NUMBER: 30,162  
; REFERENCE/DOCKET NUMBER: 00246/168001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 542-5070  
; TELEFAX: (617) 542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 180:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
US-08-488-379-180

Query Match 14.5%; Score 34; DB 2; Length 20;  
Best Local Similarity 50.0%; Pred. No. 2.8e+02;  
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 7 GPPGVDLYRLEK 18  
|||:|:|  
Db 1 GPPKLDIRKEEK 12

## RESULT 25

US-08-475-399A-180  
; Sequence 180, Application US/08475399A  
; Patent No. 6509033  
; GENERAL INFORMATION:  
; APPLICANT: Urban, Robert G.  
; APPLICANT: Chicz, Roman M.  
; APPLICANT: Vignali, Dario A.A.  
; APPLICANT: Hedley, Mary L.  
; APPLICANT: Stern, Lawrence J.  
; APPLICANT: Strominger, Jack L.  
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
; NUMBER OF SEQUENCES: 276  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson, P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: US  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows95  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/475,399A  
; FILING DATE: 07-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/077,255  
; FILING DATE: 15-JUN-1993  
; APPLICATION NUMBER: 07/925,460  
; FILING DATE: 11-AUG-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fraser, Janis K.  
; REGISTRATION NUMBER: 34,819  
; REFERENCE/DOCKET NUMBER: 00246/168003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/542-507  
; TELEFAX: 617/542-890  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 180:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-475-399A-180

Query Match 14.5%; Score 34; DB 4; Length 20;  
Best Local Similarity 50.0%; Pred. No. 2.8e+02;  
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 7 GPPGVDLYRLEK 18  
|||:|:|  
Db 1 GPPKLDIRKEEK 12

Search completed: October 31, 2005, 18:11:39  
Job time : 45 secs

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GenCore version 5.1.1.6  
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OM protein ~ protein search, using sw model

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Run on:      October 31, 2005, 18:02:02 ; Search time 163 Seconds
            (without alignments)
            115.411 Million cell updates
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**Title:** US-09-503-387-3 COPY 44 88

Perfect score: 234

Sequence: 1 VTLRCQGP PGVDLYRLEKLS.....DQAVLFIPAMKRS LAGRYRC 45

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1865214 seqs, 418043040 residues

Total number of hits satisfying chosen parameters: 524576

Minimum DB seq length: 0

Maximum DB seq	length: 0
Maximum DB seq	length: 46

Post-processing: Minimum Match 0%

Post-processing: Minimum Match 0%  
Maximum Match 100%

Maximum match 100%  
Listing first 100 summaries

Database : Published Applications AA:★

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2:	/cgn2_6/ptodata/2/pubpaa/ECT_NEW_PUB.pcp:
3:	/cgn2_6/ptodata/2/pubpaa/US05_NEW_PUB.pcp:
4:	/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pcp:
5:	/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pcp:
6:	/cgn2_6/ptodata/2/pubpaa/ECT05_PUBCOMB.pcp:
7:	/cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pcp:
8:	/cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pcp:
9:	/cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pcp:
10:	/cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pcp:
11:	/cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pcp:
12:	/cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pcp:
13:	/cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pcp:
14:	/cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pcp:
15:	/cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pcp:
16:	/cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pcp:
17:	/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pcp:
18:	/cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pcp:
19:	/cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pcp:
20:	/cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pcp:
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22:	/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pcp:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	216	92.3	41	9	US-09-832-312-6	Sequence 6, Appli
2	216	92.3	41	11	US-09-829-495-6	Sequence 6, Appli
3	92.3	92.3	41	16	US-10-850-034-6	Sequence 6, Appli
4	164	70.1	41	9	US-09-832-312-22	Sequence 22, Appl
5	164	70.1	41	11	US-09-829-495-22	Sequence 22, Appl
6	164	70.1	41	16	US-10-850-034-22	Sequence 22, Appl
7	81	34.6	19	14	US-10-446-826-20	Sequence 20, Appl
8	81	34.6	19	16	US-10-446-826-20	Sequence 20, Appl
9	80	34.2	19	14	US-10-446-826-14	Sequence 14, Appl
10	80	34.2	19	16	US-10-446-826-14	Sequence 14, Appl
11	69	29.5	19	14	US-10-446-826-21	Sequence 21, Appl

85 41 17.5 38 15 US-10-352-786-4429 Sequence 4429, Ap  
86 41 17.5 38 15 US-10-352-786-4449 Sequence 4449, Ap  
87 41 17.5 39 15 US-10-352-786-13 Sequence 13, Appl  
88 41 17.5 46 16 US-10-767-701-31630 Sequence 31630, A  
89 40 17.1 30 18 US-10-792-582-289 Sequence 289, App  
90 40 17.1 33 16 US-10-425-115-352261 Sequence 352261,  
91 40 17.1 34 15 US-10-352-786-3949 Sequence 3949, Ap  
92 40 17.1 35 15 US-10-352-786-4109 Sequence 4109, Ap  
93 40 17.1 36 15 US-10-352-786-4237 Sequence 4237, Ap  
94 40 17.1 37 15 US-10-352-786-4305 Sequence 4305, Ap  
95 40 17.1 37 15 US-10-352-786-4333 Sequence 4333, Ap  
96 40 17.1 37 15 US-10-352-786-4401 Sequence 4401, Ap  
97 40 17.1 38 15 US-10-352-786-4465 Sequence 4465, Ap  
98 40 17.1 39 15 US-10-352-786-29 Sequence 29, Appl  
99 40 17.1 45 15 US-10-424-599-184737 Sequence 184737,  
100 39 16.7 25 15 US-10-382-240-3 Sequence 3, Appl

## ALIGNMENTS

RESULT 1  
US-09-832-312-6  
; Sequence 6, Application US/09832312  
; Patent No. US20010049829A1  
; GENERAL INFORMATION:  
; APPLICANT: Busfield et al.  
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF  
; FILE REFERENCE: 7853-234  
; CURRENT APPLICATION NUMBER: US/09/832,312  
; CURRENT FILING DATE: 2001-04-09  
; PRIOR APPLICATION NUMBER: 09/610,118  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: 09/503,387  
; PRIOR FILING DATE: 2000-02-14  
; PRIOR APPLICATION NUMBER: 09/454,824  
; PRIOR FILING DATE: 1999-12-06  
; PRIOR APPLICATION NUMBER: 09/345,468  
; PRIOR FILING DATE: 1999-06-30  
; NUMBER OF SEQ ID NOS: 78  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 6  
; LENGTH: 41  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-832-312-6

Query Match 92.3%; Score 216; DB 9; Length 41;  
Best Local Similarity 100.0%; Pred. No. 2.2e-23;  
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CQPPPGVDLYRLEKLSRRYQDQAVLFIPAMKRLAGRYRC 45  
Db 1 CQPPPGVDLYRLEKLSRRYQDQAVLFIPAMKRLAGRYRC 41

RESULT 2  
US-09-829-495-6  
; Sequence 6, Application US/09829495  
; Publication No. US20040001826A1  
; GENERAL INFORMATION:  
; APPLICANT: Busfield SJ  
; APPLICANT: Villevall J  
; APPLICANT: Jandrot-Perrus M  
; APPLICANT: Vainchenker W  
; APPLICANT: Gill DS  
; APPLICANT: Qian MD  
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF  
; FILE REFERENCE: 7853-234  
; CURRENT APPLICATION NUMBER: US/09/829,495  
; CURRENT FILING DATE: 2001-04-09  
; PRIOR APPLICATION NUMBER: 09/610,118  
; PRIOR FILING DATE: 2000-06-30

; PRIOR APPLICATION NUMBER: 09/503,387  
; PRIOR FILING DATE: 2000-02-14  
; PRIOR APPLICATION NUMBER: 09/454,824  
; PRIOR FILING DATE: 1999-12-06  
; PRIOR APPLICATION NUMBER: 09/345,468  
; PRIOR FILING DATE: 1999-06-30  
; NUMBER OF SEQ ID NOS: 78  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 6  
; LENGTH: 41  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-829-495-6

Query Match 92.3%; Score 216; DB 11; Length 41;  
Best Local Similarity 100.0%; Pred. No. 2.2e-23;  
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CQPPPGVDLYRLEKLSRRYQDQAVLFIPAMKRLAGRYRC 45  
Db 1 CQPPPGVDLYRLEKLSRRYQDQAVLFIPAMKRLAGRYRC 41

RESULT 3  
US-10-850-034-6  
; Sequence 6, Application US/10850034  
; Publication No. US20040253236A1  
; GENERAL INFORMATION:  
; APPLICANT: Busfield SJ  
; APPLICANT: Villevall J  
; APPLICANT: Jandrot-Perrus M  
; APPLICANT: Vainchenker W  
; APPLICANT: Gill DS  
; APPLICANT: Qian MD  
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF  
; FILE REFERENCE: 7853-234  
; CURRENT APPLICATION NUMBER: US/10/850,034  
; CURRENT FILING DATE: 2004-05-20  
; PRIOR APPLICATION NUMBER: US/09/829,495  
; PRIOR FILING DATE: 2001-04-09  
; PRIOR APPLICATION NUMBER: 09/610,118  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: 09/503,387  
; PRIOR FILING DATE: 2000-02-14  
; PRIOR APPLICATION NUMBER: 09/454,824  
; PRIOR FILING DATE: 1999-12-06  
; PRIOR APPLICATION NUMBER: 09/345,468  
; PRIOR FILING DATE: 1999-06-30  
; NUMBER OF SEQ ID NOS: 78  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 6  
; LENGTH: 41  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-850-034-6

Query Match 92.3%; Score 216; DB 16; Length 41;  
Best Local Similarity 100.0%; Pred. No. 2.2e-23;  
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CQPPPGVDLYRLEKLSRRYQDQAVLFIPAMKRLAGRYRC 45  
Db 1 CQPPPGVDLYRLEKLSRRYQDQAVLFIPAMKRLAGRYRC 41

RESULT 4  
US-09-832-312-22  
; Sequence 22, Application US/09832312  
; Patent No. US20010049829A1  
; GENERAL INFORMATION:  
; APPLICANT: Busfield et al.  
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF  
; FILE REFERENCE: 7853-234



; CURRENT APPLICATION NUMBER: US/09/832,312  
; CURRENT FILING DATE: 2001-04-09  
; PRIOR APPLICATION NUMBER: 09/610,118  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: 09/503,387  
; PRIOR FILING DATE: 2000-02-14  
; PRIOR APPLICATION NUMBER: 09/454,824  
; PRIOR FILING DATE: 1999-12-06  
; PRIOR APPLICATION NUMBER: 09/345,468  
; PRIOR FILING DATE: 1999-06-30  
; NUMBER OF SEQ ID NOS: 78  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 22  
; LENGTH: 41  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-832-312-22

Query Match 70.1%; Score 164; DB 9; Length 41;  
Best Local Similarity 73.2%; Pred. No. 6.7e-16;  
Matches 30; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 5 CCGPGVDLYRLEKLSRSSRYQDQAVLFIPAMKRSIAGRYRC 45  
||||| ||||||| :||| ||||| |||||  
DB 1 CCGPPDVLRYRLEKLPKPKYEDQDFLFIPTMERSNAGRYRC 41

## RESULT 5

US-09-829-495-22  
; Sequence 22, Application US/09829495  
; Publication No. US20040001826A1  
; GENERAL INFORMATION:  
; APPLICANT: Busfield SJ  
; APPLICANT: Villevall J  
; APPLICANT: Jandrot-Perrus M  
; APPLICANT: Vainchenker W  
; APPLICANT: Gill DS  
; APPLICANT: Qian MD  
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF  
; FILE REFERENCE: 7853-234  
; CURRENT APPLICATION NUMBER: US/09/829,495  
; CURRENT FILING DATE: 2001-04-09  
; PRIOR APPLICATION NUMBER: 09/610,118  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: 09/503,387  
; PRIOR FILING DATE: 2000-02-14  
; PRIOR APPLICATION NUMBER: 09/454,824  
; PRIOR FILING DATE: 1999-12-06  
; PRIOR APPLICATION NUMBER: 09/345,468  
; PRIOR FILING DATE: 1999-06-30  
; NUMBER OF SEQ ID NOS: 78  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 22  
; LENGTH: 41  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-829-495-22

Query Match 70.1%; Score 164; DB 11; Length 41;  
Best Local Similarity 73.2%; Pred. No. 6.7e-16;  
Matches 30; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 5 CCGPGVDLYRLEKLSRSSRYQDQAVLFIPAMKRSIAGRYRC 45  
||||| ||||||| :||| ||||| |||||  
DB 1 CCGPPDVLRYRLEKLPKPKYEDQDFLFIPTMERSNAGRYRC 41

## RESULT 6

US-10-850-034-22  
; Sequence 22, Application US/10850034  
; Publication No. US2004025326A1  
; GENERAL INFORMATION:  
; APPLICANT: Busfield SJ

; APPLICANT: Villevall J  
; APPLICANT: Jandrot-Perrus M  
; APPLICANT: Vainchenker W  
; APPLICANT: Gill DS  
; APPLICANT: Qian MD  
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF  
; FILE REFERENCE: 7853-234  
; CURRENT APPLICATION NUMBER: US/10/850,034  
; CURRENT FILING DATE: 2004-05-20  
; PRIOR APPLICATION NUMBER: US/09/829,495  
; PRIOR FILING DATE: 2001-04-09  
; PRIOR APPLICATION NUMBER: 09/610,118  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: 09/503,387  
; PRIOR FILING DATE: 2000-02-14  
; PRIOR APPLICATION NUMBER: 09/454,824  
; PRIOR FILING DATE: 1999-12-06  
; PRIOR APPLICATION NUMBER: 09/345,468  
; PRIOR FILING DATE: 1999-06-30  
; NUMBER OF SEQ ID NOS: 78  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 22  
; LENGTH: 41  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-850-034-22

Query Match 70.1%; Score 164; DB 16; Length 41;  
Best Local Similarity 73.2%; Pred. No. 6.7e-16;  
Matches 30; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 5 CCGPGVDLYRLEKLSRSSRYQDQAVLFIPAMKRSIAGRYRC 45  
||||| ||||||| :||| ||||| |||||  
DB 1 CCGPPDVLRYRLEKLPKPKYEDQDFLFIPTMERSNAGRYRC 41

## RESULT 7

US-10-446-826-20  
; Sequence 20, Application US/10446826  
; Publication No. US20030186685A1  
; GENERAL INFORMATION:  
; APPLICANT: TANDON, NARENDRA N.  
; APPLICANT: SUN, BING  
; APPLICANT: NAKAMURA, TAKASHI  
; APPLICANT: YAMAMOTO, NAOMASA  
; TITLE OF INVENTION: PLATELET MEMBRANE GLYCOPROTEIN VI (GPVI) DNA AND  
; TITLE OF INVENTION: PROTEIN SEQUENCES, AND USES THEREOF  
; FILE REFERENCE: 03459.0026-00000  
; CURRENT APPLICATION NUMBER: US/10/446,826  
; CURRENT FILING DATE: 2003-05-29  
; PRIOR APPLICATION NUMBER: US/09/653,255B  
; PRIOR FILING DATE: 2000-08-31  
; PRIOR APPLICATION NUMBER: PCT/US00/23975  
; PRIOR FILING DATE: 2000-09-01  
; PRIOR APPLICATION NUMBER: 60/152,197  
; PRIOR FILING DATE: 1999-09-01  
; PRIOR APPLICATION NUMBER: 60/158,251  
; PRIOR FILING DATE: 1999-10-08  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 20  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-446-826-20

Query Match 34.6%; Score 81; DB 14; Length 19;  
Best Local Similarity 89.5%; Pred. No. 0.00024;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 18 KLSSRSRYQDQAVLFIPAMK 36  
||||| ||||||| |||||  
DB 1 KLSSRSRYQDQAVLFIPMAK 19

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US-10-446-826-14
Query Match          34.2%;   Score 80;   DB 14;   Length 19;
Best Local Similarity 84.2%;   Pred.No. 0.00033;
Matches 16;   Conservative 0;   Mismatches 3;   Indels 0;   Gaps 0;

QY 18 KLSSRYQDQAVLFIPAMK 36
   ||| ||||| ||||| |||||
Db 1 KLDXXRYQDQAVLFIPAMK 19

RESULT 10
US-10-446-826-14
; Sequence 14, Application US/10446826
; Publication No. US20040152628A9
; GENERAL INFORMATION:
; APPLICANT: TANDON, NARENDRA N.
; APPLICANT: SUN, BING
; APPLICANT: NAKAMURA, TAKASHI
; APPLICANT: YAMAMOTO, NAOMASA
; TITLE OF INVENTION: PLATELET MEMBRANE GLYCOPROTEIN VI (GPVI) DNA AND
; FILE REFERENCE: 03459.0026-00000
; CURRENT APPLICATION NUMBER: US/10/446,826
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: US/09/653,255B
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: PCT/US00/23975
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/152,197
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: 60/158,251
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-446-826-20
Query Match          34.6%;   Score 81;   DB 16;   Length 19;
Best Local Similarity 89.5%;   Pred.No. 0.00024;
Matches 17;   Conservative 0;   Mismatches 2;   Indels 0;   Gaps 0;

QY 18 KLSSRYQDQAVLFIPAMK 36
   ||| ||||| ||||| |||||
Db 1 KLDXXRYQDQAVLFIPAMK 19

RESULT 9
US-10-446-826-14
; Sequence 14, Application US/10446826
; Publication No. US20030186885A1
; GENERAL INFORMATION:
; APPLICANT: TANDON, NARENDRA N.
; APPLICANT: SUN, BING
; APPLICANT: NAKAMURA, TAKASHI
; APPLICANT: YAMAMOTO, NAOMASA
; TITLE OF INVENTION: PLATELET MEMBRANE GLYCOPROTEIN VI (GPVI) DNA AND
; FILE REFERENCE: 03459.0026-00000
; CURRENT APPLICATION NUMBER: US/10/446,826
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: US/09/653,255B
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: PCT/US00/23975
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/152,197
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: 60/158,251
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (4)..(5)
; OTHER INFORMATION: Any amino acid
US-10-446-826-14
Query Match          34.2%;   Score 80;   DB 16;   Length 19;
Best Local Similarity 84.2%;   Pred.No. 0.00033;
Matches 16;   Conservative 0;   Mismatches 3;   Indels 0;   Gaps 0;

QY 18 KLSSRYQDQAVLFIPAMK 36
   ||| ||||| ||||| |||||
Db 1 KLDXXRYQDQAVLFIPAMK 19

RESULT 11
US-10-446-826-21
; Sequence 21, Application US/10446826
; Publication No. US20030186885A1
; GENERAL INFORMATION:
; APPLICANT: TANDON, NARENDRA N.
; APPLICANT: SUN, BING
; APPLICANT: NAKAMURA, TAKASHI
; APPLICANT: YAMAMOTO, NAOMASA
; TITLE OF INVENTION: PLATELET MEMBRANE GLYCOPROTEIN VI (GPVI) DNA AND
; FILE REFERENCE: 03459.0026-00000
; CURRENT APPLICATION NUMBER: US/10/446,826
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: US/09/653,255B
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: PCT/US00/23975
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/152,197
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: 60/158,251
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (4)..(5)
; OTHER INFORMATION: Any amino acid
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;; PRIOR FILING DATE: 1999-09-01  
;; PRIOR APPLICATION NUMBER: 60/158,251  
;; PRIOR FILING DATE: 1999-10-08  
;; NUMBER OF SEQ ID NOS: 37  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 21  
;; LENGTH: 19  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: MOD RES  
;; LOCATION: (4)-(5)  
;; OTHER INFORMATION: Any amino acid  
US-10-446-826-21

Query Match 29.5%; Score 69; DB 14; Length 19;  
Best Local Similarity 73.7%; Pred. No. 0.013;  
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 18 KLSSRYQDQAVLFIPMAK 36  
||| ||||| ||||| ||  
Db 1 KLDXXRYQDQAVLFIPMAK 19

## RESULT 12

US-10-446-826-21  
;; Sequence 21, Application US/10446826  
;; Publication No. US20040152628A9  
;; GENERAL INFORMATION:  
;; APPLICANT: TANDON, NARENDRA N.  
;; APPLICANT: SUN, BING  
;; APPLICANT: NAKAMURA, TAKASHI  
;; APPLICANT: YAMAMOTO, NAOMASA  
;; TITLE OF INVENTION: PLATELET MEMBRANE GLYCOPROTEIN VI (GPVI) DNA AND  
;; TITLE OF INVENTION: PROTEIN SEQUENCES, AND USES THEREOF  
;; FILE REFERENCE: 03459.0026-00000  
;; CURRENT APPLICATION NUMBER: US/10/446,826  
;; CURRENT FILING DATE: 2003-05-29  
;; PRIOR APPLICATION NUMBER: US/09/653,255B  
;; PRIOR FILING DATE: 2000-08-31  
;; PRIOR APPLICATION NUMBER: PCT/US00/23975  
;; PRIOR FILING DATE: 2000-09-01  
;; PRIOR APPLICATION NUMBER: 60/152,197  
;; PRIOR FILING DATE: 1999-09-01  
;; PRIOR APPLICATION NUMBER: 60/158,251  
;; PRIOR FILING DATE: 1999-10-08  
;; NUMBER OF SEQ ID NOS: 37  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 21  
;; LENGTH: 19  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: MOD RES  
;; LOCATION: (4)-(5)  
;; OTHER INFORMATION: Any amino acid  
US-10-446-826-21

Query Match 29.5%; Score 69; DB 16; Length 19;  
Best Local Similarity 73.7%; Pred. No. 0.013;  
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 18 KLSSRYQDQAVLFIPMAK 36  
||| ||||| ||||| ||  
Db 1 KLDXXRYQDQAVLFIPMAK 19

## RESULT 13

US-10-040-862-10438  
;; Sequence 10438, Application US/10040862  
;; Publication No. US20030078396A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Gaiger, Alexander

;; APPLICANT: Algate, Paul A.  
;; APPLICANT: Mannion, Jane  
;; APPLICANT: Retter, Marc  
;; APPLICANT: Corixa Corporation  
;; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy  
;; TITLE OF INVENTION: Hematological Malignancies  
;; FILE REFERENCE: 014058-013520US  
;; CURRENT APPLICATION NUMBER: US/10/040,862  
;; CURRENT FILING DATE: 2001-11-06  
;; PRIOR APPLICATION NUMBER: US 60/186,126  
;; PRIOR FILING DATE: 2000-03-01  
;; PRIOR APPLICATION NUMBER: US 60/190,479  
;; PRIOR FILING DATE: 2000-03-17  
;; PRIOR APPLICATION NUMBER: US 60/200,545  
;; PRIOR FILING DATE: 2000-04-27  
;; PRIOR APPLICATION NUMBER: US 60/200,303  
;; PRIOR FILING DATE: 2000-04-28  
;; PRIOR APPLICATION NUMBER: US 60/200,779  
;; PRIOR FILING DATE: 2000-04-28  
;; PRIOR APPLICATION NUMBER: US 60/200,999  
;; PRIOR FILING DATE: 2000-05-01  
;; PRIOR APPLICATION NUMBER: US 60/202,084  
;; PRIOR FILING DATE: 2000-05-04  
;; PRIOR APPLICATION NUMBER: US 60/206,201  
;; PRIOR FILING DATE: 2000-05-22  
;; PRIOR APPLICATION NUMBER: US 60/218,950  
;; PRIOR FILING DATE: 2000-07-14  
;; PRIOR APPLICATION NUMBER: US 60/222,903  
;; PRIOR FILING DATE: 2000-08-03  
;; PRIOR APPLICATION NUMBER: US 60/223,416  
;; PRIOR FILING DATE: 2000-08-04  
;; PRIOR APPLICATION NUMBER: US 60/223,378  
;; PRIOR FILING DATE: 2000-08-07  
;; PRIOR APPLICATION NUMBER: US 09/796,692  
;; PRIOR FILING DATE: 2001-03-01  
;; NUMBER OF SEQ ID NOS: 10467  
;; SOFTWARE: FastSeq for Windows Version 3.0  
;; SEQ ID NO 10438  
;; LENGTH: 30  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-040-862-10438

Query Match 21.4%; Score 50; DB 14; Length 30;  
Best Local Similarity 61.1%; Pred. No. 12;  
Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 28 AVLFIPIAMKSLAGRYC 45  
||| ||||| ||||| ||  
Db 11 AELEIPAVKESDAGKYC 28

## RESULT 14

US-10-057-475B-10438  
;; Sequence 10438, Application US/10057475B  
;; Publication No. US20040002068A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Gaiger, Alexander  
;; APPLICANT: Algate, Paul A.  
;; APPLICANT: Mannion, Jane  
;; APPLICANT: Clapper, Jonathan David  
;; APPLICANT: Wang, Aijun  
;; APPLICANT: Ordonez, Nadia  
;; APPLICANT: Carter, Lauren  
;; APPLICANT: McNeill, Patricia Dianne  
;; APPLICANT: Corixa Corporation  
;; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy  
;; TITLE OF INVENTION: Hematological Malignancies  
;; FILE REFERENCE: 014058-014402US  
;; CURRENT APPLICATION NUMBER: US/10/057,475B  
;; CURRENT FILING DATE: 2002-01-22  
;; PRIOR APPLICATION NUMBER: US 60/186,126  
;; PRIOR FILING DATE: 2000-03-01

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; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10979
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10438
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-057-475B-10438
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Query Match      21.4%; Score 50; DB 15; Length 30;
Best Local Similarity 61.1%; Pred. No. 12;
Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
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QY      28  AVLFIPIAMKSLAGRYRC 45
      |||:|||||:|||||:|
Db      11  AELEIPAVKESDAGKYC 28
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RESULT 15
US-10-154-884B-10438
; Sequence 10438, Application US/10154884B
; Publication No. US2004000556A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
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; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10438
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-10438
```

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Query Match      21.4%; Score 50; DB 15; Length 30;
Best Local Similarity 61.1%; Pred. No. 12;
Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
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```
QY      28  AVLFIPIAMKSLAGRYRC 45
      |||:|||||:|||||:|
Db      11  AELEIPAVKESDAGKYC 28
```

```
RESULT 16
US-10-764-324-10438
; Sequence 10438, Application US/10764324
; Publication No. US20040175739A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/764,324
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: US/10/040,862
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10438
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-764-324-10438
```

```
Query Match      21.4%; Score 50; DB 16; Length 30;
Best Local Similarity 61.1%; Pred. No. 12;
Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
```

```
QY      28  AVLFIPIAMKSLAGRYRC 45
      |||:|||||:|||||:|
Db      11  AELEIPAVKESDAGKYC 28
```

```
RESULT 17
US-10-040-862-9613
; Sequence 9613, Application US/10c40862
; Publication No. US20030078396A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9613
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-040-862-9613

Query Match      21.4%; Score 50; DB 14; Length 34;
Best Local Similarity 61.1%; Pred. No. 14;
Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      28  AVLFIIPAMKRSIAGRYRC 45
Db      11  AELEIPAVKESDAGKYC 28

RESULT 18
US-10-057-475B-9613
; Sequence 9613, Application US/10057475B
; Publication No. US20040002068A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordenez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-014402US
; CURRENT APPLICATION NUMBER: US/10/057,475B
; CURRENT FILING DATE: 2002-01-22
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; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10979
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9613
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-057-475B-9613

Query Match      21.4%; Score 50; DB 15; Length 34;
Best Local Similarity 61.1%; Pred. No. 14;
Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      28  AVLFIIPAMKRSIAGRYRC 45
Db      11  AELEIPAVKESDAGKYC 28

RESULT 19
US-10-154-884B-9613
; Sequence 9613, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
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; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 11290

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 9613

; LENGTH: 34

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-154-884B-9613

Query Match 21.4%; Score 50; DB 15; Length 34;

Best Local Similarity 61.1%; Pred. No. 14;

Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 28 AVLFIPIAKRSLAGRYRC 45

|||:|||||:|||||

Db 11 AELEIPAVKESDAGKYIC 28

RESULT 20

US-10-764-324-9613

; Sequence 9613, Application US/10764324

; Publication No. US20040175739A1

; GENERAL INFORMATION:

; APPLICANT: Gaiger, Alexander

; APPLICANT: Algate, Paul A.

; APPLICANT: Mannion, Jane

; APPLICANT: Recter, Marc

; APPLICANT: Corixa Corporation

; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy

; FILE REFERENCE: 014058-013520US

; CURRENT APPLICATION NUMBER: US/10764,324

; CURRENT FILING DATE: 2004-01-23

; PRIOR APPLICATION NUMBER: US/10/040,862

; PRIOR FILING DATE: 2001-11-06

; PRIOR APPLICATION NUMBER: US 60/186,126

; PRIOR FILING DATE: 2000-03-01

; PRIOR APPLICATION NUMBER: US 60/190,479

; PRIOR FILING DATE: 2000-03-17

; PRIOR APPLICATION NUMBER: US 60/200,545

; PRIOR FILING DATE: 2000-04-27

; PRIOR APPLICATION NUMBER: US 60/200,779

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: US 60/200,999

; PRIOR FILING DATE: 2000-05-01

; PRIOR APPLICATION NUMBER: US 60/202,084

; PRIOR FILING DATE: 2000-05-04

; PRIOR APPLICATION NUMBER: US 60/206,201

; PRIOR FILING DATE: 2000-05-22

; PRIOR APPLICATION NUMBER: US 60/218,950

; PRIOR FILING DATE: 2000-07-14

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 10467

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 9613

; LENGTH: 34

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-764-324-9613

Query Match 21.4%; Score 50; DB 16; Length 34;

Best Local Similarity 61.1%; Pred. No. 14;

Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 28 AVLFIPIAKRSLAGRYRC 45

|||:|||||:|||||

Db 11 AELEIPAVKESDAGKYIC 28

RESULT 21

US-11-111-953-330

; Sequence 330, Application US/11111953

; Publication No. US2005021484A1

; GENERAL INFORMATION:

; APPLICANT: Moore et al.

; FILE REFERENCE: P2008P1C2

; CURRENT APPLICATION NUMBER: US/11/111,953

; CURRENT FILING DATE: 2005-04-22

; PRIOR APPLICATION NUMBER: 10/219,793

; PRIOR FILING DATE: 2002-08-16

; PRIOR APPLICATION NUMBER: 09/209,452

; PRIOR FILING DATE: 1998-12-11

; PRIOR APPLICATION NUMBER: PCT/US98/12125

; PRIOR FILING DATE: 1998-06-11

; PRIOR APPLICATION NUMBER: 60/049,547

; PRIOR FILING DATE: 1997-06-13

; PRIOR APPLICATION NUMBER: 60/049,548

; PRIOR FILING DATE: 1997-06-13

; PRIOR APPLICATION NUMBER: 60/049,549

; PRIOR FILING DATE: 1997-06-13

; PRIOR APPLICATION NUMBER: 60/049,550

; PRIOR FILING DATE: 1997-06-13

; PRIOR APPLICATION NUMBER: 60/049,566

; PRIOR FILING DATE: 1997-06-13

; PRIOR APPLICATION NUMBER: 60/049,606

; PRIOR FILING DATE: 1997-06-13

; PRIOR APPLICATION NUMBER: 60/049,607

; PRIOR FILING DATE: 1997-06-13

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 737

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 330

; LENGTH: 15

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-111-953-330

Query Match 20.9%; Score 49; DB 20; Length 15;

Best Local Similarity 57.1%; Pred. No. 7.2;

Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CRGPGVGVQTFRLR 14

|||:|||||:|||||

Db 1 CRGPGVGVQTFRLR 14

RESULT 22

US-09-815-626-13

; Sequence 13, Application US/09815626

; Patent No. US20020076752A1

; GENERAL INFORMATION:

; APPLICANT: Glucksmann, Maria Alexandra

; TITLE OF INVENTION: 3395, A NOVEL HUMAN LEUCINE-RICH REPEAT

; FILE REFERENCE: 10448-031001

; CURRENT APPLICATION NUMBER: US/09/815,626

; CURRENT FILING DATE: 2001-03-23

; PRIOR APPLICATION NUMBER: US 60/191,863

; PRIOR FILING DATE: 2000-03-24

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 13

; LENGTH: 45

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: consensus sequence

US-09-815-626-13

Query Match 19.9%; Score 46.5; DB 9; Length 45;

Best Local Similarity 34.7%; Pred. No. 63;

Matches 17; Conservative 0; Mismatches 19; Indels 13; Gaps 2;



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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 31, 2005, 17:55:59 ; Search time 38 Seconds  
(without alignments)  
113.941 Million cell updates/sec

Title: US-09-503-387-3\_COPY\_44\_88

Perfect score: 234

Sequence: 1 VTLRCQGPFGVDLYRLEKLS.....DQAVLFIPMKRSLAGRYRC 45

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 10717

Minimum DB seq length: 0  
Maximum DB seq length: 46

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : PIR\_79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	21.4	42	2 T07474	hypothetical prote
2	38	16.2	42	2 A00269	hypothetical prote
3	36	15.4	39	2 B81912	hypothetical prote
4	35.5	15.2	40	2 JT0515	Ig heavy chain V-I
5	35	15.0	29	2 A05272	gelsolin, cytosoli
6	34	14.5	31	2 S49191	hypothetical prote
7	33.5	14.3	45	2 E95058	hypothetical prote
8	33	14.1	15	2 PH0772	T-cell receptor be
9	33	14.1	43	2 B57484	cell division cont
10	32.5	13.9	33	2 B58512	bromosleeper pepti
11	32	13.7	30	2 A56790	annexin, isoform P
12	32	13.7	36	2 S49315	MSL leader peptide
13	32	13.7	36	2 S45088	probable leader pe
14	32	13.7	36	2 A25028	erythromycin resis
15	32	13.7	39	2 F64718	hypothetical prote
16	32	13.7	43	2 S24180	histone H1.a, test
17	32	13.7	45	2 T07502	hypothetical prote
18	31.5	13.5	38	2 E95080	hypothetical prote
19	31	13.2	16	2 C49048	T-cell receptor be
20	31	13.2	33	2 B29541	big gastrin - Chin
21	31	13.2	39	2 A46662	collagen alpha 2(V
22	31	13.2	41	2 E82544	hypothetical prote
23	31	13.2	42	2 JT0516	Ig heavy chain V-I
24	31	13.2	43	2 S13581	collagen alpha 1(I
25	30.5	13.0	38	2 F82485	hypothetical prote
26	30.5	13.0	41	2 AH1890	hypothetical prote
27	30.5	13.0	45	2 F86607	L36 ribosomal prot
28	30.5	13.0	45	2 B72017	L36 ribosomal prot
29	30.5	13.0	45	2 F71470	probable L36 ribos

30	30	12.8	19	2	JP0057	ribosomal protein
31	30	12.8	20	2	JP0056	ribosomal protein
32	30	12.8	28	2	I60364	phosphorybosylpyro
33	30	12.8	31	2	A25629	cytochrome-c oxida
34	30	12.8	36	2	H82427	hypothetical prote
35	30	12.8	38	2	G70236	hypothetical prote
36	30	12.8	38	2	B47753	beta-defensin-11 -
37	30	12.8	39	2	B81897	hypothetical prote
38	30	12.8	41	2	S50091	DNA-directed DNA p
39	30	12.8	43	2	A37091	60K staloalprotein h
40	30	12.8	44	2	S77931	exoskeletal protei
41	30	12.8	45	2	A80749	hypothetical prote
42	29.5	12.6	32	2	F90807	hypothetical prote
43	29.5	12.6	32	2	B85667	hypothetical prote
44	29.5	12.6	32	2	A64848	hypothetical prote
45	29.5	12.6	38	2	A05222	anthranilate phosph
46	29.5	12.6	38	2	A61070	pituitary adenylat
47	29.5	12.6	38	2	A91655	pituitary adenylat
48	29.5	12.6	40	2	S45688	glutathione transf
49	29.5	12.6	41	2	T15832	hypothetical prote
50	29	12.4	12	2	PH1635	Ig H chain V-D-J r
51	29	12.4	18	4	I56393	lacZ/IS1 mutant fu
52	29	12.4	20	2	S50175	kallikrein (PK-120
53	29	12.4	24	2	B56978	collagen alpha 2(X
54	29	12.4	31	2	S03297	Ig alpha chain C r
55	29	12.4	31	2	S03295	Ig alpha chain C r
56	29	12.4	34	2	D81044	hypothetical prote
57	29	12.4	35	2	A64733	hypothetical prote
58	29	12.4	38	2	C82373	hypothetical prote
59	29	12.4	39	2	A38623	collagen alpha 1(I
60	29	12.4	41	2	S26936	Ig heavy chain V r
61	29	12.4	43	2	S11111	Ig heavy chain V r
62	29	12.4	44	2	PC2242	cytochrome c554 -
63	29	12.4	46	2	T42016	ppl-like Ser/Thr p
64	28.5	12.2	31	2	C82851	hypothetical prote
65	28.5	12.2	40	1	SWFGS	sausage - sauge
66	28.5	12.2	44	2	T19161	hypothetical prote
67	28	12.0	9	2	S26508	collagen alpha 2(V
68	28	12.0	12	2	A61360	vespakinin M - hor
69	28	12.0	18	2	S02175	acrosin (EC 3.4.21
70	28	12.0	20	2	JP0059	ribosomal protein
71	28	12.0	20	2	JP0060	ribosomal protein
72	28	12.0	20	2	JP0061	ribosomal protein
73	28	12.0	20	2	JU0330	hypothetical prote
74	28	12.0	20	2	A99091	hypothetical prote
75	28	12.0	21	2	S16073	alanine-tRNA ligas
76	28	12.0	23	2	JP0082	ribosomal protein
77	28	12.0	23	2	A61574	hyaluronic acid-bi
78	28	12.0	28	2	A60752	outer membrane pro
79	28	12.0	30	2	A18136	17K antigen - Rick
80	28	12.0	36	1	WISMAA	alpha-amylase inhi
81	28	12.0	37	2	AG0540	hypothetical prote
82	28	12.0	39	2	H82657	hypothetical prote
83	28	12.0	40	1	W4BP17	gene 4.1 protein -
84	28	12.0	40	2	T03831	hypothetical prote
85	28	12.0	41	2	G59484	hypothetical prote
86	28	12.0	43	2	B81995	hypothetical prote
87	28	12.0	43	2	E82246	hypothetical prote
88	27.5	11.8	27	2	A61071	pituitary adenylat
89	27.5	11.8	31	2	C95215	hypothetical prote
90	27.5	11.8	35	2	B95157	hypothetical prote
91	27.5	11.8	39	2	S00490	RNA-binding protei
92	27	11.5	8	2	PT0559	T-cell receptor be
93	27	11.5	10	2	S26506	collagen alpha 1(V
94	27	11.5	14	2	S00150	ovostatin - duck (
95	27	11.5	17	2	A27636	cytotoxin B - Clo
96	27	11.5	20	2	PQ0544	capsid protein VP5
97	27	11.5	21	2	A60235	pyruvate dehydroge
98	27	11.5	23	2	C56978	collagen alpha 1(I
99	27	11.5	24	2	T50123	peroxisomal target
100	27	11.5	26	2	S11629	elastin precursor

## ALIGNMENTS

A;Molecule type: DNA  
A;Residues: 1-39 <PAR>  
A;Cross-references: UNIPROT:Q9JU98; GB:AL162755; GB:AL157959; NID:97379742; PIDN:CAB84665  
A;Experimental source: serogroup A, strain Z2491  
C;Genetics:  
A;Gene: NMA1426

C; Species: *Oenothera lamarckiana* (Onagraceae); Black pine/  
C; Date: 14-May-1999 #sequence revision 14-May-1999 #text\_change 09-Jul-2004  
C; Accession: T07474  
R; Wakasugi, T.; Tsudzuki, J.; Ito, S.; Nakashima, K.; Tsudzuki, T.; Sugiura, M.  
Proc. Natl. Acad. Sci. U.S.A. 91, 9794-9798, 1994  
A; Title: Loss of all nrd genes as determined by sequencing the entire chloroplast genome  
A; Reference number: Z16030; MUID:95024047; PMID:7937893

A;Accession: J01471  
A;Status: preliminary; translated from GE/EMBL/DBDB  
A;Molecule type: DNA  
A;Residues: 1-42 <WAK>  
A;Cross-references: UNIPROT:Q32948; EMBL:D17510; NID:G529643; PIDN:BA04352.1; PID:G1262  
C;Genetics:  
C;Genome: chloroplast  
C;Keywords: chloroplast

Query Match	21.4%	Score 50;	DB 2;	Length 42;
Best Local Similarity	41.7%	Pred. No.	6.2;	
Matches 10;	Conservative	7;	Mismatches	7;
Indels	0;	Gaps	0;	

```
QY      19 LSSRYQDQAVLFIPAMKRSLAGR 42  
       :| : |: |: |: |: |: |:  
Db      1 MSIEKERDRMILFLPAVILSLFGR 24
```

RESULT 2  
AD0269  
hypothetical protein YPO2210 [imported] - Yersinia pestis (strain C092)  
C:Species: Yersinia pestis  
C:Date: 02-Nov-2001 #sequence\_revision 03-Nov-2001 #text\_change 09-Jul-2004  
C:Accession: AD0269  
R:Parkhill, J.; Wen, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Iarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Hill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall, Nature 413, 523-527, 2001  
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
A:Reference number: AB0001; MUID:21470413; PMID:11586360

A;Accession: P08793  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-42 <KUR>  
A;Cross-references: UNIPROT:Q8ZEG3; GB:AL590842; PIDN:CAC91016.1; PID:g15980210; GSPDB:GSPDB:G15980210  
C;Genetics:  
A;Gene: YPO2210

Query Match	16.2%	Score 38;	DB 2;	Length 42;
Best Local Similarity	35.3%	Pred. No.	2.8e+02;	
Matches	6;	Mismatches	3;	Indels 0;
Conservative		Gaps	0;	

```

QY      10 GVDLYRLEKLSRRYQD 26
      |||:| : :|:|:|:|:|:|
Db      12 GVDIYLVNQLTSTQVRE 28

```

RESULT 3  
B81912  
hypothetical protein NMA1426 [imported] - *Neisseria meningitidis* (strain Z2491 serogroup  
C;Species: *Neisseria meningitidis*  
C;Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 09-Jul-2004  
C;Accession: B81912  
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel  
S.; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,  
Nature 404, 502-506, 2000  
A;Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.  
A;Reference number: A81775; MUID:20222556; PMID:10761919  
A;Accession: B81912  
A;Status: preliminary

Query Match 15.0%; Score 35; DB 2; Length 29;  
Best Local Similarity 37.5%; Pred. No. 4.8e+02;  
Matches 6; Conservative 5; Mismatches 5; Indels

Qy 3 LRCQPPGVDLYRLEK 18  
|: ||: ::||  
Db 8 LKAGKQPLQIWRVEK 23

RESULT 6  
S49191  
hypothetical protein 6 - *Azotobacter vinelandii* (fragment)

34351  
hypothetical protein 6 - *Azotobacter vinelandii* (fragment)

C:Species: Azotobacter vinelandii  
C:Date: 16-Feb-1995 #sequence\_revision 12-May-1995 #text\_change 09-Jul-2004  
C:Accession: S49191  
R:Wientjens, R.; van Dongen, W.; Haaker, H.  
Submitted to the EMBL Data Library, April 1992  
A:Description: Molecular cloning of fixA, fixB, fixC and fixX genes of Azotobacter vinelandii  
A:Reference number: S49186  
A:Accession: S49191  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-31 <WIE>  
A:Cross-references: UNIPROT:Q44509; EMBL:X65515

Query Match 14.5%; Score 34; DB 2; Length 31;  
Best Local Similarity 50.0%; Pred. No. 7.1e+02;  
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 15 RLEKLSRRYQDQA 28  
DB 13 QLEKESARRYEBLA 26

RESULT 7  
B5058  
Hypothetical protein SP0504 [imported] - Streptococcus pneumoniae (strain TIGR4)  
C:Species: Streptococcus pneumoniae  
C:Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 09-Jul-2004  
C:Accession: E95058  
R:Tetzelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heidorn, J.D.; Unayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, N.; Hickey, E.K.; Holt, I.E.  
Science 293, 498-506, 2001  
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A.; Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.  
A:Reference number: A95000; MUID:21357209; PMID:11463916  
A:Accession: E95058  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-45 <KUR>  
A:Cross-references: UNIPROT:Q97584; GB:AE005672; PIDN:AAK74662.1; PID:g14971977; GSPDB:C  
C:Genetics:  
A:Experimental source: strain TIGR4  
A:Gene: SP0504

Query Match 14.3%; Score 33.5; DB 2; Length 45;  
Best Local Similarity 33.3%; Pred. No. 1.2e+03;  
Matches 8; Conservative 6; Mismatches 7; Indels 3; Gaps 2;

QY 5 CQG--PPGVDLRLKLSRRYQD 26  
DB 14 CQGENPEDIEFYD-EQLQAEKVED 36

RESULT 8  
PH0772  
T-cell receptor beta chain (J4) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 05-Nov-1999  
C:Accession: PH0772  
R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.  
J. Exp. Med. 174, 1371-1383, 1991  
A:Title: T cell receptor genes in a series of class I major histocompatibility complex-1 allelic exclusion and antigen-specific repertoire.  
A:Reference number: PH0746; MUID:92078846; PMID:1836010  
A:Accession: PH0772  
A:Molecule type: mRNA  
A:Residues: 1-15 <CAS>  
A:Cross-references: EMBL:X60866; NID:g52749; PIDN:CAA43256.1; PID:g52750  
A:Experimental source: T lymphocyte  
C:Keywords: T-cell receptor

Query Match 14.1%; Score 33; DB 2; Length 15;  
Best Local Similarity 66.7%; Pred. No. 4.5e+02;

Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 20 SSSRYDQAVLP 31  
DB 3 SSRRDRDQAPLF 14

RESULT 9  
B57484  
call division control protein CDC37 homolog splice form 2 - chicken (fragment)  
C:Species: Gallus gallus (chicken)  
C:Date: 19-Jan-1996 #sequence\_revision 19-Jan-1996 #text\_change 09-Jul-2004  
C:Accession: B57484  
R:Grammatikakis, N.; Grammatikakis, A.; Yoneda, M.; Yu, Q.; Banerjee, S.D.; Toole, B.P.  
J. Biol. Chem. 270, 16198-16205, 1995  
A:Title: A novel glycosaminoglycan-binding protein is the vertebrate homologue of the cell surface heparan sulfate proteoglycan core protein.  
A:Reference number: A57484; MUID:95332325; PMID:7608185  
A:Accession: B57484  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-43 <GRA>  
A:Cross-references: UNIPROT:Q90653; GB:U25026  
C:Keywords: alternative splicing

Query Match 14.1%; Score 33; DB 2; Length 43;  
Best Local Similarity 34.5%; Pred. No. 1.4e+03;  
Matches 10; Conservative 4; Mismatches 15; Indels 0; Gaps 0;

QY 1 VTLRCQPPGVDLRLKLSRRYQDQAV 29  
DB 1 VVQRCGCPVVGETHGQAGRASEHRDQAV 29

RESULT 10  
B58512  
bromosleeper peptide - cone shell (Conus radiatus)  
C:Species: Conus radiatus (radial cone)  
C:Date: 19-Mar-1997 #sequence\_revision 11-Apr-1997 #text\_change 16-Aug-2004  
C:Accession: B58512  
R:Craig, A.G.; Jimenez, E.C.; Dykert, J.; Nielsen, D.B.; Gulyas, J.; Abogadie, F.C.; Port J. Biol. Chem. 272, 4689-4698, 1997  
A:Title: A novel post-translational modification involving bromination of tryptophan. Identification of the brominated residue.  
A:Reference number: A58512; MUID:97184108; PMID:9030520  
A:Accession: B58512  
A:Molecule type: protein  
A:Residues: 1-33 <CRA>  
A:Cross-references: UNIPROT:P58804  
C:Keywords: bromine; carboxylglutamic acid; hydroxyproline; toxin; venom  
F:1/Modified site: 6-bromotryptophan (Trp) #status experimental  
F:6.8.9.29/Modified site: gamma-carboxyglutamic acid (Glu) #status experimental  
F:21/Modified site: 4-hydroxyproline (Pro) #status atypical  
F:22/Modified site: 4-hydroxyproline (Pro) #status experimental

Query Match 13.9%; Score 32.5; DB 2; Length 33;  
Best Local Similarity 63.6%; Pred. No. 1.2e+03;  
Matches 7; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 1 VTLR-CQPPG 10  
DB 13 VTFKTCQPPG 23

RESULT 11  
A56790  
annexin, isoform P34 - tomato (fragment)  
C:Species: Lycopersicon esculentum (tomato)  
C:Date: 03-Nov-1995 #sequence\_revision 03-Nov-1995 #text\_change 09-Jul-2004  
C:Accession: A56790  
R:Smallwood, M.F.; Gurr, S.J.; McPherson, M.J.; Roberts, K.; Bowles, D.J.  
Biochem. J. 281, 501-505, 1992  
A:Title: The pattern of plant annexin gene expression.  
A:Reference number: A56790; MUID:92143819; PMID:1736896

A;Accession: A56790  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-30 <SWA>  
A;Cross-references: UNIPROT:Q40139; GB:X63996; GB:S79791; NID:q19173; PIDN:CAA45402.1; F  
A;Note: sequence extracted from NCBI backbone (NCBIN:79791, NCBIP:79793)  
C;Superfamily: annexin 1; annexin repeat homology

Query Match 13.7%; Score 32; DB 2; Length 30;  
Best Local Similarity 30.0%; Pred. No. 1.3e+03;  
Matches 6; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Qy 17 EKLSSRYQDAVLFTPAWK 36  
||| ||| ||| |||  
Db 1 EKISDKAYSDELIRILSR 20

RESULT 12  
S49315  
MSL leader peptide 1 - Enterococcus hirae  
N;Alternate names: probable erythromycin resistance protein 1  
C;Species: Enterococcus hirae  
C;Date: 16-Feb-1995 #sequence\_revision 12-May-1995 #text\_change 18-Jun-1999  
C;Accession: S49315  
R;Raze, D.; Coyette, J.; Ghuyssen, J.M.  
submitted to the EMBL Data Library, September 1994  
A;Reference number: S49315  
A;Accession: S49315  
A;Molecule type: DNA  
A;Residues: 1-36 <RAZ>  
A;Cross-references: EMBL:X91655; NID:G551433; PIDN:CAA57313.1; PID:G551434  
A;Experimental source: strain S185  
C;Superfamily: MSL leader peptide

Query Match 13.7%; Score 32; DB 2; Length 36;  
Best Local Similarity 38.9%; Pred. No. 1.6e+03;  
Matches 7; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 16 LEKLSSRYQDAVLFTIP 33  
||| ||| ||| |||  
Db 16 LKTKNSDYADKYVRLIP 33

RESULT 13  
S45088  
Probable leader peptide ermI - Streptococcus pyogenes plasmid pDB101 and pBT233  
N;Alternate names: ermI protein; erythromycin resistance protein ermI  
C;Species: Streptococcus pyogenes  
C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 16-Aug-2004  
C;Accession: S45088; S68608  
R;Ceglowski, P.; Boitsov, G.; Lueder, G.; Alonso, J.C.  
submitted to the EMBL Data Library, June 1992  
A;Reference number: S45072  
A;Accession: S45088  
A;Molecule type: DNA  
A;Residues: 1-36 <CEG>  
A;Cross-references: EMBL:X66468; NID:G496500; PIDN:CAA47094.1; PID:G496517  
A;Experimental source: plasmid pDB101  
A;Genetics: G1  
R;Ceglowski, P.; Boitsov, A.; Chai, S.; Alonso, J.C.  
Gene 136, 1-12, 1993  
A;Title: Analysis of the stabilization system of pSM19035-derived plasmid pBT233 in Bacil  
A;Reference number: S68600; MUID:94123985; PMID:8293991  
A;Accession: S68608  
A;Molecule type: DNA  
A;Residues: 1-36 <CE2>  
A;Cross-references: EMBL:X64695; NID:G456362; PIDN:CAA45936.1; PID:G456371  
A;Experimental source: plasmid pBT233  
A;Genetics: G2  
C;Genetics: <G1>  
A;Gene: ermI  
A;Genome: plasmid pDB101  
C;Genetics: <G2>

A;Gene: ermI  
A;Genome: plasmid pBT233

Query Match 13.7%; Score 32; DB 2; Length 36;  
Best Local Similarity 38.9%; Pred. No. 1.6e+03;  
Matches 7; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 16 LEKLSSRRYQDQAVLFIP 33  
|::|||:  
DB 16 LKQTKNSDYADKYVRLIP 33

RESULT 14  
A25028  
erythromycin resistance protein, ORF1 - Enterococcus faecalis  
N;Alternate names: macrolide-lincosamide-streptogramin B-resistance protein  
C;Species: Enterococcus faecalis  
C;Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 09-Jul-2004  
C;Accession: A25028  
R;Shaw, J.H.; Clewell, D.B.  
J. Bacteriol. 164, 782-796, 1985  
A;Title: Complete nucleotide sequence of macrolide-lincosamide-streptogramin B-resistance  
A;Reference number: A91808; MUID:86033641; PMID:2997130  
A;Accession: A25028  
A;Molecule type: DNA  
A;Residues: 1-36 <SHA>  
A;Cross-references: UNIPROT:P23130  
C;Superfamily: unassigned leader peptides

Query Match 13.7%; Score 32; DB 2; Length 36;  
Best Local Similarity 38.9%; Pred. No. 1.6e+03;  
Matches 7; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 16 LEKLSSRRYQDQAVLFIP 33  
|::|||:  
DB 16 LKQTKNSDYADKYVRLIP 33

RESULT 15  
F64718  
hypothetical protein HP1590 - Helicobacter pylori (strain 26695)  
C;Species: Helicobacter pylori  
C;Date: 09-Aug-1997 #sequence\_revision 09-Aug-1997 #text\_change 09-Jul-2004  
C;Accession: F64718  
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney, son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.W.; Fujii, C.; Bowman, C.; Wathey, L. Nature 388, 539-547, 1997  
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.N.  
A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.  
A;Reference number: A64520; MUID:97394467; PMID:9252185  
A;Accession: F64718  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-39 <TOM>  
A;Cross-references: UNIPROT:O26108; GB:AE000656; GB:AE000511; NID:g2314771; PIDN:AAD08629;

Query Match 13.7%; Score 32; DB 2; Length 39;  
Best Local Similarity 53.3%; Pred. No. 1.7e+03;  
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 12 DLVLEKLSSRRYQD 26  
|||::|||:  
DB 8 DLFLKRLSSSDLKD 22

RESULT 16  
S24180  
histone H1.a, testis - rat (fragments)  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 02-Dec-1993 #sequence\_revision 26-Jul-1996 #text\_change 26-Jul-1996  
C;Accession: S24180  
R;Baubichon-Cortay, H.; Mallet, L.; Denoroy, L.; Roux, B.

Biochim. Biophys. Acta 1122, 167-177, 1992

A>Title: Histone H1a subtype presents structural differences compared to other histone H1 subtypes  
A:Reference number: S23924; MUID:92353102; PMID:1643090  
A:Accession: S24180  
A:Molecule type: protein  
A:Residues: 1-33,34-43 <BAU>  
C:Superfamily: histone H1

Query Match 13.7%; Score 32; DB 2; Length 43;  
Best Local Similarity 32.0%; Pred. No. 1.9e+03;  
Matches 8; Conservative 11; Mismatches 4; Indels 2; Gaps 1;

QY 16 LEKLSSRYQDOAVLFIPAMKRSIA 40  
          :::|::: : : : |:::|  
DB 3 VQAVSSKK--ERSGVSLAAALKKSIA 25  
          :::|::: : : : |:::|

RESULT 17

T07502

Hypothetical protein 45d - Japanese black pine chloroplast  
C:Species: Chloroplast Pinus thunbergiana (Japanese black pine)  
C>Date: 14-May-1999 #sequence\_revision 14-May-1999 #text\_change 09-Jul-2004  
C:Accession: T07502  
R:Wakaugi, T.; Tsudzuki, J.; Ito, S.; Nakashima, K.; Tsudzuki, T.; Sugiura, M.  
Proc. Natl. Acad. Sci. U.S.A. 91, 9794-9798, 1994  
A>Title: Loss of all ndh genes as determined by sequencing the entire chloroplast genome  
A:Reference number: Z16030; MUID:95024047; PMID:7937893  
A:Accession: T07502  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-45 <WAK>  
A:Cross-references: UNIPROT:Q32964; EMBL:D17510; NID:g529643; PIDN:BAAA04380.1; PID:g1262  
C:Genetics:  
A:Genome: chloroplast  
C:Keywords: chloroplast

Query Match 13.7%; Score 32; DB 2; Length 45;  
Best Local Similarity 31.6%; Pred. No. 2e+03;  
Matches 12; Conservative 5; Mismatches 13; Indels 8; Gaps 2;

QY 1 VTLCRCGPPGVDLVRLKLSRRYQDOAVLFIPAMKRS 38  
          :::|:::|:::|:::|:::|:::|:::|  
DB 15 ITIR-----DQORLRANKMEPFQFWA-LFLPGRGS 44  
          :::|:::|:::|:::|:::|:::|:::

RESULT 18

E95080

Hypothetical protein SP0693 [imported] - Streptococcus pneumoniae (strain TIGR4)  
C:Species: Streptococcus pneumoniae  
C>Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 09-Jul-2004  
C:Accession: E95080  
R:Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heidison, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, C.; Hickey, E.K.; Holt, I.E.  
Science 293, 498-506, 2001  
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A.; Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.  
A:Reference number: A95000; MUID:21357203; PMID:11463916  
A:Accession: E95080  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-38 <KUR>  
A:Cross-references: UNIPROT:Q9TRU4; GB:AEO05672; PIDN:AAK74838.1; PID:g14972169; GSPDB:G  
A:Experimental source: strain TIGR4  
C:Genetics:  
A:Gene: SP0693

Query Match 13.5%; Score 31.5; DB 2; Length 38;  
Best Local Similarity 30.8%; Pred. No. 1.9e+03;  
Matches 8; Conservative 7; Mismatches 10; Indels 1; Gaps 1;

QY 18 KLSSRYQDOAVLFIPAMKRS-LAGR 42  
          :::|:::|:::|:::|:::|:::|:::



Search completed: October 31, 2005, 18:02:38  
Job time : 42 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 31, 2005, 17:55:59 ; Search time 173 Seconds  
(without alignments)  
133.200 Million cell updates/sec

Title: US-09-503-387-3\_COPY\_44\_88

Perfect score: 234

Sequence: 1 VTLRCQPPGVLDYRLEKLS.....DQAVLFIPMKRSLAGRYRC 45

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 60209

Minimum DB seq length: 0

Maximum DB seq length: 46

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52	22.2	36	2 Q6Q4B9	Q6Q4B9 taetes min
2	50	21.4	42	2 Q32948	Q32948 pinus thunb
3	41.5	17.7	35	2 Q8KYK6	Q8KYK6 bacillus an
4	41.5	17.7	35	2 Q6EZM2	Q6EZM2 bacillus an
5	41	17.5	41	2 Q64CY7	Q64CY7 uncultured
6	39.5	16.9	41	2 Q8EXK8	Q8EXK8 leptospira
7	39.5	16.9	46	2 Q8VU04	Q8VU04 streptococc
8	39	16.7	32	2 Q725Z6	Q725Z6 desulfovibr
9	38.5	16.5	42	2 Q8E8U0	Q8E8U0 shewanella
10	38	16.2	32	2 Q72FU1	Q72FU1 desulfovibr
11	38	16.2	39	2 Q70UV9	Q70UV9 myoxus gliis
12	38	16.2	42	2 Q66AJ8	Q66AJ8 yersinia ps
13	38	16.2	42	2 Q8ZEG3	Q8ZEG3 yersinia pe
14	38	16.2	46	2 Q7S7T8	Q7S7T8 neurospora
15	37.5	16.0	46	2 Q70UI8	Q70UI8 uncultured
16	37	15.8	42	2 Q93305	Q93305 chaenocepha
17	37	15.8	42	2 Q93306	Q93306 chionodrac
18	36	15.4	25	2 Q70WF0	Q70WF0 aeromonas s
19	36	15.4	28	2 Q9TRM4	Q9TRM4 bos taurus
20	36	15.4	37	2 Q732X8	Q732X8 bacillus ce
21	36	15.4	39	2 Q9JU98	Q9JU98 neisseria m
22	36	15.4	45	2 Q8L6S4	Q8L6S4 gossypium h
23	35.5	15.2	38	2 Q75W88	Q75W88 eriocheir j
24	35	15.0	29	2 Q7M2V6	Q7M2V6 oryctolagus
25	35	15.0	30	2 Q9R892	Q9R892 chlamydia t
26	35	15.0	37	2 Q8CLI7	Q8CLI7 yersinia pe
27	35	15.0	40	2 Q9QWC8	Q9QWC8 rattus sp.
28	35	15.0	41	2 Q72A24	Q72A24 desulfovibr
29	35	15.0	43	2 Q9LI94	Q9LI94 human papil
30	35	15.0	44	1 YL53_SCHPO	Q8CF95 schizosacch
31	34.5	14.7	35	2 Q8F4R5	Q8F4R5 leptospira

32	34.5	14.7	45	2	Q83WQ0	Q83WQ0 shigella bo
33	34	14.5	17	2	Q71UQ2	Q71UQ2 homo sapien
34	34	14.5	32	2	Q44509	Q44509 azotobacter
35	34	14.5	39	2	Q05821	Q05821 saccharomyc
36	34	14.5	39	2	Q9PVG7	Q9PVG7 xiphophorus
37	34	14.5	43	2	Q7UUD2	Q7UUD2 rhodospirill
38	34	14.5	45	2	Q7QV81	Q7QV81 giardia lam
39	33.5	14.3	41	2	Q69DR1	Q69DR1 drosophila
40	33.5	14.3	45	2	Q8L6G9	Q8L6G9 posidonio o
41	33.5	14.3	45	2	Q97S84	Q97S84 streptococ
42	33	14.1	31	2	Q73KQ7	Q73KQ7 treponema d
43	33	14.1	32	2	Q7M6V2	Q7M6V2 mus musculu
44	33	14.1	35	2	Q7S2W2	Q7S2W2 neurospora
45	33	14.1	37	2	Q73DU6	Q73DU6 bacillus ce
46	33	14.1	40	2	Q6NFR5	Q6NFR5 corynebacte
47	33	14.1	46	2	Q9QX77	Q9QX77 rattus norv
48	32.5	13.9	33	1	CX8W_CONRA	P58804 conus radia
49	32.5	13.9	38	2	Q8IU36	Q8IU36 periplaneta
50	32.5	13.9	38	2	Q8IU37	Q8IU37 sepioteuthi
51	32.5	13.9	38	2	Q8IU38	Q8IU38 hydra magni
52	32.5	13.9	38	2	Q8IU39	Q8IU39 dugesia jap
53	32.5	13.9	38	2	Q75W94	Q75W94 halocynthia
54	32.5	13.9	38	2	Q75W87	Q75W87 oncorhynch
55	32.5	13.9	38	2	Q75W90	Q75W90 sardinops m
56	32.5	13.9	38	2	Q75W92	Q75W92 stephanolep
57	32.5	13.9	38	2	Q8AYP4	Q8AYP4 acipenser s
58	32.5	13.9	38	2	Q8AYP5	Q8AYP5 trachurus j
59	32	13.7	30	2	Q739F3	Q739F3 bacillus ce
60	32	13.7	32	2	Q9BPX8	Q9BPX8 homo sapien
61	32	13.7	35	2	Q8EBZ5	Q8EBZ5 shewanella
62	32	13.7	35	2	Q800I7	Q800I7 human immun
63	32	13.7	36	2	Q9UE39	Q9UE39 homo sapien
64	32	13.7	36	2	Q83U72	Q83U72 streptococ
65	32	13.7	36	2	Q83WK8	Q83WK8 enterococc
66	32	13.7	36	2	Q77664	Q77664 human immun
67	32	13.7	37	2	Q49100	Q49100 mycoplasma
68	32	13.7	38	2	Q75W93	Q75W93 cyprinus ca
69	32	13.7	39	2	Q8TE27	Q8TE27 homo sapien
70	32	13.7	39	2	Q26108	Q26108 helicobacte
71	32	13.7	40	2	Q62GT2	Q62GT2 burkholderi
72	32	13.7	40	2	Q8PCU1	Q8PCU1 xanthomonas
73	32	13.7	41	2	Q6C589	Q6C589 yarrowia li
74	32	13.7	42	2	Q7RCZ1	Q7RCZ1 plasmodium
75	32	13.7	43	2	Q937G6	Q937G6 klebsiella
76	32	13.7	44	2	Q81IV8	Q81IV8 bacillus ce
77	32	13.7	44	2	Q87N11	Q87N11 vibrio para
78	32	13.7	45	2	Q32964	Q32964 pinus thunb
79	31.5	13.5	32	2	Q9TSQ0	Q9TSQ0 cercopithe
80	31.5	13.5	38	2	Q97RU4	Q97RU4 streptococ
81	31.5	13.5	38	2	Q75W86	Q75W86 lampetra ja
82	31.5	13.5	39	2	Q9MZF7	Q9MZF7 bos taurus
83	31.5	13.5	41	2	Q6SF91	Q6SF91 uncultured
84	31.5	13.5	45	2	Q9NQ49	Q9NQ49 homo sapien
85	31	13.2	16	2	Q9QUW5	Q9QUW5 rattus sp.
86	31	13.2	20	2	Q9QUW3	Q9QUW3 pyrococcus
87	31	13.2	23	2	Q9TWJ9	Q9TWJ9 mytilus edu
88	31	13.2	31	2	Q9TWK5	Q9TWK5 mytilus edu
89	31	13.2	31	2	Q9TT24	Q9TT24 sus scrofa
90	31	13.2	33	1	GAST_CHIBR	P10034 chinchilla
91	31	13.2	33	2	Q9TWD8	Q9TWD8 carausius m
92	31	13.2	36	2	Q72WS2	Q72WS2 desulfovibr
93	31	13.2	37	2	Q8EIQ2	Q8EIQ2 shewanella
94	31	13.2	37	2	Q8EXV9	Q8EXV9 leptospira
95	31	13.2	38	2	Q8CQ09	Q8CQ09 staphylococ
96	31	13.2	39	2	Q8EGP4	Q8EGP4 shewanella
97	31	13.2	41	2	Q9PAH7	Q9PAH7 xylella fas
98	31	13.2	42	2	Q9T0Z2	Q9T0Z2 bacterioph
99	31	13.2	42	2	Q50817	Q50817 mycobacteri
100	31	13.2	43	2	Q6WRF9	Q6WRF9 bos taurus

ALIGNMENTS



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Query Match 17.7%; Score 41.5; DB 2; Length 35;
Best Local Similarity 35.7%; Pred. No. 2.9e+02;
Matches 10; Conservative 6; Mismatches 9; Indels 3; Gaps 1;

QY 10 GVDLYRLEKLSRRYQDQAVLPIPAKR 37
DQ 10 GVDLYRLEKLSRRYQDQAVLPIPAKR 37
DB 10 GVDLYRLEKLSRRYQDQAVLPIPAKR 37

RESULT 5
Q64CY7 PRELIMINARY; PRT; 41 AA.
AC Q64CY7;
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=GZ19C8_1;
OS uncultured archaeon GZfos19C8.
OC Archaea; environmental samples.
OX NCBI_TaxID=285361;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15353801;
RA Hallam S.J., Putnam N., Preston C.M., Dettler J.C., Rokhsar D.,
Richardson P.M., DeLong E.F.;
RT "Reverse methanogenesis: testing the hypothesis with environmental
genomics.";
RL Science 305:1457-1462 (2004).
RN [2]
RP SEQUENCE FROM N.A.
RA Putnam N., Dettler J.C., Richardson P.M., Rokhsar D.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY714831; AAU82740.1;
KW Hypothetical protein.
FT NON_TER 41
SQ SEQUENCE 41 AA; 4694 MW; 0F9614E2EC88F247 CRC64;

Query Match 17.5%; Score 41; DB 2; Length 41;
Best Local Similarity 61.5%; Pred. No. 4.1e+02;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 10 GVDLYRLEKLSRRYQDQAVLPIPAKR 37
DQ 10 GVDLYRLEKLSRRYQDQAVLPIPAKR 37
DB 10 GVDLYRLEKLSRRYQDQAVLPIPAKR 37

RESULT 6
Q8EXK8 PRELIMINARY; PRT; 41 AA.
AC Q8EXK8;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=L8200;
OS Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=173;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
RC MEDLINE=22598143; PubMed=12712204; DOI=10.1038/nature01597;
RA Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,
Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,
Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,
Xu J.-G., Zhao G.-P.;
RT "Unique physiological and pathogenic features of Leptospira
interrogans revealed by whole-genome sequencing.";
RL Nature 422:888-893 (2003).
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DR EMBL: AE011608; AAN51759.1; -.
KW Complete proteome.
SQ SEQUENCE 41 AA; 5047 MW; ACAD816676B4C9A5 CRC64;

Query Match 16.9%; Score 39.5; DB 2; Length 41;
Best Local Similarity 33.3%; Pred. No. 6.7e+02;
Matches 9; Conservative 6; Mismatches 9; Indels 3; Gaps 1;

QY 6 QGPGVDLYRLEKLSRRYQDQAVLPI 32
DQ 6 QGPGVDLYRLEKLSRRYQDQAVLPI 32
DB 3 QNPEKISFLNMEKISNCREKD---LFL 26

RESULT 7
Q8VU04 PRELIMINARY; PRT; 46 AA.
AC Q8VU04;
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Cps6BL (Fragment).
GN Name=cps6BL;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RA Griffiths D.B., Hall L.M.C.; EMBL/GenBank/DBJ databases.
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF298581; AAL68438.1; -.
DR HSSP; Q9HU22; 1FXO.
DR GO: GO:0016779; F:nucleotidyltransferase activity; IEA.
DR GO: GO:0009058; P:biocynthesis; IEA.
DR Pfam; PF00483; NTP_transferase; 1.
FT NON_TER 46
SQ SEQUENCE 46 AA; 5002 MW; E77C585696887F8C CRC64;

Query Match 16.9%; Score 39.5; DB 2; Length 46;
Best Local Similarity 28.9%; Pred. No. 7.7e+02;
Matches 11; Conservative 7; Mismatches 17; Indels 3; Gaps 1;

QY 7 GPGVDLYRLEKLSRRYQDQAVLPIPAKRSLAG 41
DQ 7 GPGVDLYRLEKLSRRYQDQAVLPIPAKRSLAG 41
DB 8 GSGGTRLYPLTRAASKQLMPVVDKPMIYYPSTLMLAG 45

RESULT 8
Q725Z6 PRELIMINARY; PRT; 32 AA.
AC Q725Z6;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=DVU3277;
OS Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB
8303).
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
OC Desulfovibrionaceae; Desulfovibrio.
OX NCBI_TaxID=882;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15077118; DOI=10.1038/nbt959;
RA Heidelberg J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T.,
RA Kolonay J.F., Eisen J.A., Ward N.B., Methe B.A., Brinkac L.M.,
RA Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R.,
RA Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J.,
RA Peterson J.D., Davidsen T.M., Zafar N., Zhou L., Radune D.,
Dimitrov G., Hance M., Tran K., Khouri H.M., Gill J., Utterback T.R.,
RA Feldblyum T.V., Wall J.D., Voordouw G., Fraser C.M.;
RT "The genome sequence of the anaerobic, sulfate-reducing bacterium
Desulfovibrio vulgaris Hildenborough.";
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RL  Nat. Biotechnol. 22:554-559 (2004).
DR  EMBL; AE017320; AAS97747.1; -.
DR  TIGR; DVU01277; -.
KW  Complete proteome; Hypothetical protein.
SQ  SEQUENCE 32 AA; 3525 MW; F53FF15367E2F8 CRC64;

Query Match      16.7%; Score 39; DB 2; Length 32;
Best Local Similarity 36.8%; Pred. No. 5.9e+02;
Matches 7; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY  15 RLKLSRRYQDQAVLPI 33
Db  11 KLDTLGAESYQEQVLNVP 29

RESULT 9
Q8E8U0  SEQUENCE FROM N.A.
ID  Q8E8U0  PRELIMINARY; PRT; 42 AA.
AC  Q8E8U0;
DT  01-MAR-2003 (TrEMBLrel. 23, Created)
DT  01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT  01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE  Hypothetical protein S04566.
GN  OrderedLocuNames=S04566;
OS  Shewanella oneidensis.
OC  Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC  Shewanellaceae; Shewanella.
OX  NCBI_TaxID=70863;
[1]
RN  SEQUENCE FROM N.A.
RC  STRAIN=MR-1;
RX  MDLLine=22297686; PubMed=12368813; DOI=10.1038/nbt749;
RA  Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
RA  Read T.D., Eisen J.A., Seshadri R., Ward N.L., Methe B.A.,
RA  Clayton R.A., Meyer T., Raapin A., Scott J., Beanan M.J.,
RA  Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S.,
RA  Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A.,
RA  White O., Wolf A.M., Vamathevan J.J., Weidman J.F., Impraim M.,
RA  Lee K., Berry K.J., Lee C., Mueller J., Khouri H.M., Gill J.,
RA  Uterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O.,
RA  Venter J.C., Neilson K.H., Fraser C.M.;
RT  "Genome sequence of the dissimilatory metal ion-reducing bacterium
RT  Shewanella oneidensis."
RL  Nat. Biotechnol. 20:1118-1123 (2002).
DR  EMBL; AE015889; AAN57527.1; -.
DR  TIGR; S04566; -.
KW  Complete proteome; Hypothetical protein.
SQ  SEQUENCE 42 AA; 4713 MW; 5A9329C540A6BC99 CRC64;

Query Match      16.5%; Score 38.5; DB 2; Length 42;
Best Local Similarity 50.0%; Pred. No. 9.5e+02;
Matches 9; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY  28 AVLFIIPAKRS-LAGRYR 44
Db  19 AILFVYAMKNTIGRLR 36

RESULT 10
Q72FU1  SEQUENCE FROM N.A.
ID  Q72FU1  PRELIMINARY; PRT; 32 AA.
AC  Q72FU1;
DT  05-JUL-2004 (TrEMBLrel. 27, Created)
DT  05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT  05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE  Hypothetical protein.
GN  OrderedLocuNames=DVU0122;
OS  Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB
OS  8303).
OC  Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
OC  Desulfovibrionaceae; Desulfovibrio.
OX  NCBI_TaxID=882;
[1]
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RP  SEQUENCE FROM N.A.
RX  PubMed=15077118; DOI=10.1038/nbt959;
RA  Heidelberg J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T.,
RA  Kolonay J.F., Eisen J.A., Ward N.L., Methe B.A., Brinkac L.M.,
RA  Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R.,
RA  Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J.,
RA  Peterson J.D., Daviden T.M., Zafar N., Zhou L., Radune D.,
RA  Dimitrov G., Hance M., Tran K., Khouri H.M., Gill J., Uterback T.R.,
RA  Feldblyum T.V., Wall J.D., Voordouw G., Fraser C.M.;
RT  "The genome sequence of the anaerobic, sulfate-reducing bacterium
RT  Desulfovibrio vulgaris Hildenborough."
RL  Nat. Biotechnol. 22:554-559 (2004).
DR  EMBL; AE017309; AAS94606.1; -.
DR  TIGR; DVU0122; -.
KW  Complete proteome.
SQ  SEQUENCE 32 AA; 3592 MW; 9BDDFD1775E5EDAA CRC64;

Query Match      16.2%; Score 38; DB 2; Length 32;
Best Local Similarity 50.0%; Pred. No. 8.1e+02;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY  17 EKLSSRRYQDQAVLPI 32
Db  5 KSLSKRRQDAIVVFL 20

RESULT 11
Q70UV9  SEQUENCE FROM N.A.
ID  Q70UV9  PRELIMINARY; PRT; 39 AA.
AC  Q70UV9;
DT  05-JUL-2004 (TrEMBLrel. 27, Created)
DT  05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT  05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE  B-spectrin 1 (Fragment).
GN  Name=spbn;
OS  Myoxus glis (Fat dormouse) (Glis glis).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Myoxidae; Myoxinae;
OC  Myoxus.
OX  NCBI_TaxID=41261;
[1]
RN  SEQUENCE FROM N.A.
RP  Montgelard C., Matthee C.A., Robinson T.J.;
RL  Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AJ536391; CAD66170.1; -.
DR  NON_TER 1 1
FT  NON_TER 39 39
SQ  SEQUENCE 39 AA; 4520 MW; E6FA42DC59F1A9C CRC64;

Query Match      16.2%; Score 38; DB 2; Length 39;
Best Local Similarity 33.3%; Pred. No. 1e+03;
Matches 7; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY  23 RYQDQAVLFIIPAMKRSAGRY 43
Db  8 RWGSQAPTFLPCVKQATSPAY 28

RESULT 12
Q66AJ8  SEQUENCE FROM N.A.
ID  Q66AJ8  PRELIMINARY; PRT; 42 AA.
AC  Q66AJ8;
DT  25-OCT-2004 (TrEMBLrel. 28, Created)
DT  25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT  25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE  Hypothetical protein.
GN  ORFNames=YPTB2132;
OS  Versinia pseudotuberculosis IP 32953.
OC  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC  Enterobacteriaceae; Versinia.
OX  NCBI_TaxID=273123;
[1]
RN  SEQUENCE FROM N.A.
```

Eukaryota; Fungi; Ascomycota; Peziizomycotina; Sordariomycetes;  
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.  
NCBI\_TaxID=5141;  
[1]  
SEQUENCE FROM N.A.  
RC STRAIN=OR74A;  
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,  
RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Putcell S., Rehman B.,  
RA Elkins T., Engels P., Wang S., Nielsen C.B., Butler J., Endrizzi M.,  
RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,  
RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,  
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,  
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,  
RA Kamal M., Kamysuselis M., Mauceli E., Bielke C., Rudd S., Frishman D.,  
RA Kryzofova S., Rasmussen C., Metzner R.L., Perkins D.D., Kroken S.,  
RA Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmari S.A.,  
RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,  
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,  
RA Natvig D.O., Alex L.A., Mannheim G., Ebbole D.J., Freitag M.,  
RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;  
RL "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";  
RT Nature 0:0-0(2003).  
CC - CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL: AA001000271; EAA32077.1; -.  
SQ SEQUENCE 46 AA; 4780 MW; 9E9CE767B13820B0 CRC64;

Query Match 16.2%; Score 38; DB 2; Length 46;  
Best Local Similarity 57.1%; Pred No. 1.2e+03;  
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 31 FIPAKRSLAGRYR 44  
:-: ||| |

Db 28 FLTWTMSISLVGRYR 41

RESULT 15

Q70UI8 PRELIMINARY; PRT; 46 AA.

ID Q70UI8  
AC Q70UI8;  
DT 05-JUL-2004 (TEMBUREl. 27, Created)  
DI 05-JUL-2004 (TEMBUREl. 27, Last sequence update)  
DT 05-JUL-2004 (TEMBUREl. 27, Last annotation update)  
DE Laccase (EC 1.10.3.2) (Fragment).  
GN Nameslac;  
OS uncultured basidiomycete.  
OC Eukaryota; Fungi; Basidiomycota; environmental samples.  
OX NCBI\_TaxID=175244;  
[1]  
SEQUENCE FROM N.A.  
RP Luis P., Walther G., Kellner H., Martin F., Buscot F.;  
RA "Diversity of laccase genes from basidiomycetes in a forest soil.";  
RT Soil Biol. Biochem. 36:1025-1036(2004).  
RL  
DR EMBL: AJ540275; CAD62538.1; -.  
DR HSPG; Q9Y780; IA65.  
DR GO: GO:0008471; F:laccase activity; IEA.  
DR GO: GO:0016491; F:oxygenoreductase activity; IEA.  
DR InterPro: IPR008972; Cupredoxin.  
KW Oxidoreductase.  
FT NON\_TER 1  
FT NON\_TER 46  
SQ SEQUENCE 46 AA; 5430 MW; F104400E14C16B7 CRC64;

Query Match 16.0%; Score 37.5; DB 2; Length 46;  
Best Local Similarity 31.8%; Pred No. 1.5e+03;  
Matches 7; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

QY 4 RCQGPGVDL-YRLEXLSSRY 24  
:-: ||| |

Db 21 QCRIIPCKSWTYRFQALQTGF 42

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RESULT 16
O93305 ID O93305 PRELIMINARY; PRT; 42 AA.
AC O93305;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Alpha globin (Fragment).
OS Chaenocephalus aceratus (White crocodile fish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
OC Notothenicoidei; Channichthyidae; Chaenocephalus.
OX NCBI_TaxID=36190;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98278981; PubMed=9614073; DOI=10.1074/jbc.273.24.14745;
RA Zhao Y., Ratnayake-Lecamwasam M., Parker S.K., Cocco E.,
RA Camardella L., di Prisco G., Detrich H.W. III.;
RT "The major adult alpha-globin gene of antarctic teleosts and its
RT remnants in the hemoglobinless icefishes. Calibration of the
RT mutational clock for nuclear genes."
RL J. Biol. Chem. 273:14745-14752(1998).
DR EMBL; AF049914; AAC25098.1; -.
DR HSP; P45718; IIA6.
DR GO; GO:0005344; F: oxygen transporter activity; IEA.
DR GO; GO:0015671; P: oxygen transport; IEA.
DR GO; GO:0006810; P: transport; IEA.
DR InterPro; IPR000971; Globin-like.
DR InterPro; IPR009050; Globin-like.
DR Pfam; PF00042; Globin; 1.
DR PROSITE; PS01033; GLOBIN; 1.
KW Heme; Oxygen transport; Transport.
FT NON_TER 1 1
SQ SEQUENCE 42 AA; 4734 MW; F499AE047B991E35 CRC64;

Query Match 15.8%; Score 37; DB 2; Length 42;
Best Local Similarity 57.1%; Pred. No. 1.5e+03;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 31 FIPAMKRSLAGRYR 44
| : : : : :
Db 29 FLSAVALSLADRYR 42

RESULT 17
O93306 ID O93306 PRELIMINARY; PRT; 42 AA.
AC O93306;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Alpha globin (Fragment).
OS Chionodraco rasbospinosus (Ocellated icefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
OC Notothenicoidei; Channichthyidae; Chionodraco.
OX NCBI_TaxID=34790;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98278981; PubMed=9614073; DOI=10.1074/jbc.273.24.14745;
RA Zhao Y., Ratnayake-Lecamwasam M., Parker S.K., Cocco E.,
RA Camardella L., di Prisco G., Detrich H.W. III.;
RT "The major adult alpha-globin gene of antarctic teleosts and its
RT remnants in the hemoglobinless icefishes. Calibration of the
RT mutational clock for nuclear genes."
RL J. Biol. Chem. 273:14745-14752(1998).
DR EMBL; AF049915; AAC25099.1; -.
DR HSP; P45718; IIA6.
DR GO; GO:0005344; F: oxygen transporter activity; IEA.
DR GO; GO:0015671; P: oxygen transport; IEA.
DR GO; GO:0006810; P: transport; IEA.

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DR InterPro; IPR000971; Globin.
DR InterPro; IPR009050; Globin-like.
DR Pfam; PF00042; Globin; 1.
DR PROSITE; PS01033; GLOBIN; 1.
KW Heme; Oxygen transport; Transport.
FT NON_TER 1 1
SQ SEQUENCE 42 AA; 4734 MW; F499AE047B991E35 CRC64;

Query Match 15.8%; Score 37; DB 2; Length 42;
Best Local Similarity 57.1%; Pred. No. 1.5e+03;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 31 FIPAMKRSLAGRYR 44
| : : : : :
Db 29 FLSAVALSLADRYR 42

RESULT 18
Q70WF0 ID Q70WF0 PRELIMINARY; PRT; 25 AA.
AC Q70WF0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein (Fragment).
OS Aeromonas salmonicida.
OG Plasmid pAR-32.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=645;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Ar-32;
RA Sorum H., L'Abée-Lund T.M., Solberg A., Wold A.;
RT "The integron containing IncU R plasmids PRAS1 and pAR-32 from the
RT fish pathogen Aeromonas salmonicida."
RL Antimicrob. Agents Chemother. 47:1285-1290(2003).
DR EMBL; AJ517791; CAD57203.1; -.
KW Hypothetical protein; Plasmid.
FT NON_TER 25 25
SQ SEQUENCE 25 AA; 2603 MW; 9D7CE3384EC28E9D CRC64;

Query Match 15.4%; Score 36; DB 2; Length 25;
Best Local Similarity 61.5%; Pred. No. 1.1e+03;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 33 PAMKRSLAGRYR 45
| : : : : :
Db 7 PVASRSIAVRPRC 19

RESULT 19
Q9TRM4 ID Q9TRM4 PRELIMINARY; PRT; 28 AA.
AC Q9TRM4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Vesicular amine transporter (fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=93028536; PubMed=1357668;
RA Stern-Bach Y., Keen J.N., Bejerano M., Steiner-Mordoch S., Wallach M.,
RA Findlay J.B., Schuldiner S.;
RT "Homology of a vesicular amine transporter to a gene conferring
RT resistance to 1-methyl-4-phenylpyridinium."
RL Proc. Natl. Acad. Sci. U.S.A. 89:9730-9733(1992).
SQ SEQUENCE 28 AA; 3357 MW; A70D254C5C8A8346 CRC64;

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Query Match      15.4%; Score 36; DB 2; Length 28;
Best Local Similarity 38.1%; Pred. No. 1.3e+03;
Matches      8; Conservative      4; Mismatches      9; Indels      0; Gaps      0;

QY      12 DLYRLEKLSRRYQDQAVLF 32
      :|||:|||:
Db      3 ELALLRLOESRHSRXLILFI 23

RESULT 20
Q732X8      PRELIMINARY;      PRT;      37 AA.
AC      Q732X8;
DT      05-JUL-2004 (TReMBLrel. 27, Created)
DT      05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT      05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE      Hypothetical protein.
GN      OrderedLocusNames=BCE3782;
OS      Bacillus cereus (strain ATCC 10987).
OC      Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX      NCBI_TaxID=222523;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      PubMed=14960714; DOI=10.1093/nar/gkh258;
RA      Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
RA      Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,
RA      Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
RT      "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
RT      adaptations and a large plasmid related to Bacillus anthracis pXOI.";
RL      Nucleic Acids Res. 32:977-988(2004).
DR      EMBL; AE017276; AAS42687.1; -.
DR      TIGR; BCE3782; -.
KW      Complete proteome; Hypothetical protein.
SQ      SEQUENCE      37 AA; 4474 MW; 1F0A43DD20620FE CRC64;

Query Match      15.4%; Score 36; DB 2; Length 37;
Best Local Similarity 31.0%; Pred. No. 1.8e+03;
Matches      9; Conservative      5; Mismatches      7; Indels      8; Gaps      1;

QY      5 COGPGVDLYRLEKLSRRYQDQAVLFI 33
      :|||:|||:
Db      3 CEGN-----EKQSTKKKRVRLFFP 23

RESULT 21
Q9JU98      PRELIMINARY;      PRT;      39 AA.
AC      Q9JU98;
DT      01-OCT-2000 (TReMBLrel. 15, Created)
DT      01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT      01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE      Hypothetical protein NMA1426.
GN      OrderedLocusNames=NMA1426;
OS      Neisseria meningitidis (serogroup A).
OC      Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC      Neisseriaceae; Neisseria.
OX      NCBI_TaxID=65699;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      STRAIN=22491 / Serogroup A / Serotype 4A;
RX      MEDLINE=20222556; PubMed=10761919; DOI=10.1038/35006655;
RA      Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,
RA      Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA      Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
RA      Jagsis K., Leather S., Moule S., Mungall K.L., Quail M.A.,
RA      Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA      Whitehead S., Spratt B.G., Barrall B.G.;
RT      "Complete DNA sequence of a serogroup A strain of Neisseria
RT      meningitidis 22491.";
RL      Nature 404:502-506(2000).
DR      EMBL; AL162755; CAB84665.1; -.
DR      PIR; B81912; B81912.
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KW      Complete proteome; Hypothetical protein.
SQ      SEQUENCE      39 AA; 4347 MW; 78431A918706821C CRC64;

Query Match      15.4%; Score 36; DB 2; Length 39;
Best Local Similarity 47.4%; Pred. No. 1.9e+03;
Matches      9; Conservative      4; Mismatches      4; Indels      2; Gaps      1;

QY      16 LEKLSRR--YDQAVLFI 32
      :|||:|||:
Db      7 LRLSLGNRFPYLDRAISFI 25

RESULT 22
Q8L6S4      PRELIMINARY;      PRT;      45 AA.
AC      Q8L6S4;
DT      01-OCT-2002 (TReMBLrel. 22, Created)
DT      01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT      01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE      MYB101 protein (Fragment).
GN      Name=myb101;
OS      Gossypium hirsutum (Upland cotton).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC      eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
OX      NCBI_TaxID=3635;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Ovary;
RX      MEDLINE=22941922; PubMed=14580676; DOI=10.1016/j.bbexp.2003.08.009;
RA      Suo J., Liang X., Pu L., Zhang Y., Xue Y.;
RT      "Identification of GhMYB109 encoding a R2R3 MYB transcription factor
RT      that expressed specifically in fiber initials and elongating fibers of
RT      cotton (Gossypium hirsutum L.).";
RL      Biochim. Biophys. Acta 1630:25-34(2003).
CC      -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR      EMBL; AJ459116; CAD30565.1; -.
DR      HSSP; P06876; 1GV2.
DR      GO; GO:0005634; C:nucleus; IEA.
DR      GO; GO:0003677; F:DNA binding; IEA.
DR      InterPro; IPR009057; Homeodomain like.
DR      InterPro; IPR001005; MYB_DNA_binding.
DR      Pfam; PF0249; MYB_DNA-binding; 1.
DR      PROSITE; PS00090; MYB_3; 1.
KW      Nuclear protein.
FT      NON_TER      1
FT      NON_TER      45
SQ      SEQUENCE      45 AA; 5461 MW; 475F302957C492A6 CRC64;

Query Match      15.4%; Score 36; DB 2; Length 45;
Best Local Similarity 31.2%; Pred. No. 2.3e+03;
Matches      10; Conservative      4; Mismatches      6; Indels      12; Gaps      1;

QY      13 LYRLEKLSRRYQDQAVLFI 44
      :|||:|||:
Db      24 IIRLHLKLGNRWS-----LIAGRYR 43

RESULT 23
Q75W88      PRELIMINARY;      PRT;      38 AA.
AC      Q75W88;
DT      05-JUL-2004 (TReMBLrel. 27, Created)
DT      05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT      05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE      Pituitary adenylate cyclase activating polypeptide (Fragment).
OS      Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC      Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC      Eubrachyura; Grapsoidea; Varunidae; Eriocheir.
OX      NCBI_TaxID=95603;
RN      [1]
```

RP SEQUENCE FROM N.A.  
RA Hoshino M., Ogata M.;  
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AB121765; BA011231;  
KW Aminoacyl-tRNA synthetase.  
FT NON\_TER 1  
GO: GO:0005576; C:extracellular; IEA.  
DR GO: GO:0005179; F:hormone activity; IEA.  
DR InterPro; IPR000532; Glucagon.  
DR Pfam; PF00123; Hormone 2; 1.  
DR PRINTS; PR00275; GLUCAGON.  
DR SMART; SM00070; GLUCA; 1  
DR PROSITE; PS00260; GLUCAGON; 1.  
FT NON\_TER 1  
FT NON\_TER 38  
SQ SEQUENCE 38 AA; 4656 MW; BF3C9C49770AF06F CRC64;  
  
Query Match 15.2%; Score 35.5; DB 2; Length 38;  
Best Local Similarity 41.4%; Pred.No. 2.2e+03;  
Matches 12; Conservative 4; Mismatches 4; Indels 9; Gaps 2;  
  
QY 20 SSSRYQDQAVLFTPAMKRSLAG---RYR 44  
| | | | | : | | | | |  
Db 9 SYSRYEQM-----AVKKYLAAVLGKRYR 32  
| | | | | : | | | | |  
  
RESULT 24  
Q7M2V6 PRELIMINARY; PRT; 29 AA.  
AC Q7M2V6;  
DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Gelsolin, cytosolic (Fragment).  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=84185643; PubMed=6325429;  
RA Yin H.L., Kwiatkowski D.J., Mole J.E., Cole F.S.;  
RL J. Biol. Chem. 259:5271-5276(1984).  
DR PIR; A05272; A05272.  
DR HSSP; O28372; 1DON.  
FT NON\_TER 1  
FT NON\_TER 29  
SQ SEQUENCE 29 AA; 3360 MW; 378857224D94D6D2 CRC64;  
  
Query Match 15.0%; Score 35; DB 2; Length 29;  
Best Local Similarity 37.5%; Pred.No. 1.9e+03;  
Matches 6; Conservative 5; Mismatches 5; Indels 0; Gaps 0;  
  
QY 3 LRCQGPQVDLYRLEK 18  
| : | | : | : | | |  
Db 8 LKAGKQFGLQIWRVEK 23  
| : | | : | : | | |  
  
RESULT 25  
Q9R892 PRELIMINARY; PRT; 30 AA.  
AC Q9R892;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Histidinyl-tRNA synthetase (Fragment).  
GN Name=hisp;  
OS Chlamydia trachomatis.  
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
OX NCBI\_TaxID=813;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=L2 434B;  
RA Wang L., Steenburg S.D., Zheng Y., Larsen S.H.;  
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF087298; AAD04075.1; .  
KW GO: GO:0004812; F:tRNA ligase activity; IEA.  
KW Aminoacyl-tRNA synthetase.  
FT NON\_TER 1  
FT NON\_TER 30  
SQ SEQUENCE 30 AA; 3581 MW; 80328F755DA0F216 CRC64;  
  
Query Match 15.0%; Score 35; DB 2; Length 30;  
Best Local Similarity 61.5%; Pred.No. 2e+03;  
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
  
QY 12 DLYRLEKLSRSSRY 24  
| | | | | : | | | | |  
Db 1 DLDRLSLPSQERY 13  
| | | | | : | | | | |  
  
Search completed: October 31, 2005, 18:01:53  
Job time : 177 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October,29, 2005, 04:07:45 ; Search time 163 Seconds

(without alignments)  
111.520 Million cell updates/sec

Title: US-09-503-387-3\_COPY\_134\_180

Perfect score: 268

Sequence: 1 CQRYGDFQFALYKEGDPAP.....YRASFPITVTAAHSGTYRC 47

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 927287

Minimum DB seq length: 0

Maximum DB seq length: 48

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A\_Geneseq\_16Dec04.\*

1: geneseqp1980s.\*

2: geneseqp1990s.\*

3: geneseqp2000s.\*

4: geneseqp2001s.\*

5: geneseqp2002s.\*

6: geneseqp2003as.\*

7: geneseqp2003bs.\*

8: geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	268	100.0	47	4	AAB61259 Human TAN
2	268	100.0	47	6	ABU11225 Human TAN
3	220	82.1	47	4	AAB61272 Mouse TAN
4	220	82.1	47	6	ABU11238 TANGO 268
5	47.5	17.7	42	3	ABU11910 Glucagon-
6	46.5	17.4	34	7	ADM34378 Human LY1
7	46.5	17.4	38	2	AAV20266 Human ubi
8	46.5	17.4	38	2	AAV20269 Human ubi
9	45.5	17.0	44	6	ABR83767 Pseudomon
10	45.5	17.0	44	6	ADP70087 AcMA-type
11	45	16.8	24	6	ABR99764 Antigenic
12	45	16.8	30	7	ADM35220 Human LY1
13	45	16.8	41	7	ADM35348 Human LY1
14	44.5	16.6	45	4	AAU22223 Human car
15	44.5	16.6	45	7	ADP46191 Human car
16	44.5	16.6	45	8	ADJ07609 Human car
17	44	16.4	26	2	AAW22399 Soluble C
18	44	16.4	26	2	AAW75901 Recombina
19	44	16.4	26	8	ADP88820 Amino aci
20	44	16.4	30	2	AAU04273 Bovine va
21	44	16.4	42	5	ABG80828 Human SF-
22	43	16.0	13	8	ADI46793 Permeabil
23	43	16.0	13	8	ADI46809 Permeabil
24	43	16.0	13	8	ADP86970 Junctiona
25	43	16.0	13	8	ADP86986 Junctiona

26	43	16.0	14	8	ADI46794	Permeabil
27	43	16.0	14	8	ADI46810	Permeabil
28	43	16.0	14	8	ADP86971	Junctiona
29	43	16.0	14	8	ADP86987	Junctiona
30	43	16.0	17	8	ADI46788	Permeabil
31	43	16.0	17	8	ADI46804	Permeabil
32	43	16.0	17	8	ADP86965	Junctiona
33	43	16.0	17	8	ADP86981	Junctiona
34	43	16.0	19	8	ADI46789	Permeabil
35	43	16.0	19	8	ADI46805	Permeabil
36	43	16.0	19	8	ADP86982	Junctiona
37	43	16.0	19	8	ADP86966	Junctiona
38	43	16.0	28	2	AAW21973	FCR pep1.
39	43	16.0	28	2	AAW22247	FCR pep 1
40	43	16.0	28	2	AAW22247	Mouse TAN
41	43	16.0	41	6	ABU11237	Mouse TAN
42	43	16.0	42	4	AAU21124	Human nov
43	43	16.0	42	5	ABG80829	Human SF-
44	43	16.0	43	2	AAU75862	Factor XI
45	42.5	15.9	21	5	AAU76481	Antioxi
46	42	15.7	12	8	ADI46792	Permeabil
47	42	15.7	12	8	ADI46808	Permeabil
48	42	15.7	12	8	ADP86985	Junctiona
49	42	15.7	12	8	ADP86969	Junctiona
50	42	15.7	15	8	ADI46803	Permeabil
51	42	15.7	15	8	ADI46787	Permeabil
52	42	15.7	15	8	ADP86980	Junctiona
53	42	15.7	15	8	ADP86964	Junctiona
54	42	15.7	30	4	ABG50698	Human sec
55	42	15.7	30	6	ABO44955	Novel hum
56	42	15.7	30	7	ABO26435	Protein a
57	41.5	15.5	39	4	AAU31439	Novel hum
58	41	15.3	21	8	ADG70460	Alginic a
59	41	15.3	26	2	AAV19726	SEQ ID NO
60	41	15.3	39	2	AAW74059	Human npe
61	41	15.3	46	5	ABG98308	Antibody
62	41	15.3	46	5	ABG98305	Antibody
63	40.5	15.1	26	2	AAV20272	Human ubi
64	40.5	15.1	35	4	AAW20373	Peptide #
65	40.5	15.1	35	4	ABB41004	Peptide #
66	40.5	15.1	35	4	AAW34779	Peptide #
67	40.5	15.1	35	4	ABB25097	Protein #
68	40.5	15.1	35	4	AAW74664	Human bon
69	40.5	15.1	35	4	AAW61863	Human bra
70	40.5	15.1	35	5	ABG44485	Human pep
71	40.5	15.1	45	2	AAV36531	Fragment
72	40.5	15.1	45	6	ADA12079	Human nov
73	40	14.9	13	8	ADI46745	Permeabil
74	40	14.9	13	8	ADI46729	Permeabil
75	40	14.9	14	8	ADI46730	Permeabil
76	40	14.9	14	8	ADI46746	Permeabil
77	40	14.9	17	8	ADI46740	Permeabil
78	40	14.9	17	8	ADI46724	Permeabil
79	40	14.9	19	8	ADI46725	Permeabil
80	40	14.9	19	8	ADI46741	Permeabil
81	40	14.9	21	5	ADK36472	Novel hum
82	40	14.9	21	8	ADP04108	Starch sy
83	40	14.9	24	5	ABP58996	Paenibaci
84	40	14.9	26	2	AAW00918	Streptomy
85	40	14.9	26	3	AAV77199	S. venezu
86	40	14.9	36	6	ABR62506	Modified
87	39.5	14.7	41	2	AAV48270	Human pro
88	39.5	14.7	43	6	ABW73011	Staphyloc
89	39.5	14.7	47	4	AAW92023	Human dig
90	39.5	14.7	47	4	AAU20001	Human liv
91	39.5	14.7	47	5	ABP40862	Human liv
92	39.5	14.7	47	7	ADJ14980	Human liv
93	39	14.6	12	8	ADI46744	Permeabil
94	39	14.6	12	8	ADI46728	Permeabil
95	39	14.6	15	8	ADI46723	Permeabil
96	39	14.6	15	8	ADI46739	Permeabil
97	39	14.6	47	2	AAW80351	Sugi alle
98	38.5	14.4	26	3	AAW23988	Linker pe

99 38.5 14.4 30 7 ADM35219 Agm35219 Human LY1  
100 38.5 14.4 35 6 ABR62513 ABR62513 Modified

ALIGNMENTS

RESULT 1  
AAB61259  
ID AAB61259 standard; protein; 47 AA.  
XX  
AC AAB61259;  
XX  
DT 04-APR-2001 (first entry)  
XX  
DE Human TANGO 268 Ig-like domain #2.  
XX  
KW Human; TANGO 268; cardiant; cerebroprotective; cytostatic; anticoagulant;  
KW thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI;  
KW platelet membrane glycoprotein receptor; bleeding disorder;  
KW blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;  
KW ischaemia; cardiovascular disease; immunological disease; liver disorder;  
KW cancer.  
XX  
OS Homo sapiens.  
XX  
FN WO200100810-A1.  
XX  
PD 04-JAN-2001.  
XX  
PF 30-JUN-2000; 2000WO-US018152.  
XX  
PR 30-JUN-1999; 99US-00345468.  
PR 06-DEC-1999; 99US-00454824.  
PR 14-FEB-2000; 2000US-00503387.  
XX  
PA (MILL-) MILLENNIUM PHARM INC.  
XX  
PI Busfield SJ, Villelall J, Jandrot-Perrus M, Vainchencker W;  
PI Gill DS, Qian MD, Kingsbury G;  
XX  
DR WPI; 2001-080877/09.  
XX  
PT New genes encoding human platelet-expressed collagen receptor,  
PT glycoprotein VI, and its modulators, useful for preventing, treating and  
PT diagnosing hemorrhagic disorders, thrombotic diseases and immunological  
PT disorders.  
XX  
PS Disclosure; Page 203; 227pp; English.  
XX

XX The present sequence is given in a specification relating to an isolated  
CC nucleic acid molecule encoding a platelet membrane glycoprotein receptor  
CC glycoprotein VI (GPVI), also called TANGO 268. The GPVI polynucleotides  
CC and polypeptides and their modulators, e.g. antisense nucleic acids,  
CC ribozymes and antibodies, are useful for preventing, treating and  
CC diagnosing disorders associated with aberrant expression or activity of  
CC GPVI. These disorders include bleeding disorders (e.g.  
CC thrombocytopenia), blood vessel injury, thrombotic disorders (e.g.  
CC coronary artery and cerebral artery diseases (e.g. stroke and ischaemia),  
CC cardiovascular diseases (e.g. atherosclerosis and myocardial infarction),  
CC immunological diseases (e.g. platelet disorder) and embryonic liver  
CC disorders. Preferably they are used to prevent acute cardiac ischaemia  
CC following angioplasty and metastatic cancers, especially of the colon and  
CC liver  
XX  
SQ Sequence 47 AA;

Query Match 100.0%; Score 268; DB 4; Length 47;  
Best Local Similarity 100.0%; Pred. No. 2.5e-28;  
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 CQTRYGDFQALYKGDPAFYKNPWRVYRASFFIITVTAHSGTYRC 47

Db 1 CQTRYGDFQALYKGDPAFYKNPWRVYRASFFIITVTAHSGTYRC 47

RESULT 2  
ABU11225  
ID ABU11225 standard; peptide; 47 AA.  
XX  
AC ABU11225;  
XX  
DT 06-FEB-2003 (first entry)  
XX  
DE Human TANGO 268 IgG like domain #2.  
XX  
KW Human; mouse; variable heavy; VH; antigen; cancer;  
KW complementarity determining region; TANGO 268; glycoprotein VI; GPVI;  
KW TANGO 268; extracellular matrix; collagen; platelet release;  
KW proliferation; migration; embryogenesis; inflammation; thrombosis;  
KW degranulation; thrombocytopenia; antibody; thrombotic disorder;  
KW cerebral vascular disease; stroke; ischaemia; venous thromboembolism;  
KW leg swelling; pain; ulceration; pulmonary embolism; coronary disease;  
KW cardiovascular disease; angina pectoris; myocardial infarction;  
KW coronary restenosis; atherosclerosis; immunological disorder;  
KW developmental disorder; embryonic disorder; liver disorder;  
KW cerebral vascular disease; venous thromboembolism disease.  
XX  
OS Homo sapiens.  
XX  
FN WO200280968-A1.  
XX  
PD 17-OCT-2002.  
XX  
PF 09-APR-2002; 2002WO-US011122.  
XX  
PR 09-APR-2001; 2001US-00829495.  
XX  
PA (MILL-) MILLENNIUM PHARM INC.  
XX  
PI Busfield SJ, Villelall J, Jandrot-Perrus M, Vainchencker W;  
PI Gill DS, Qian DM, Kingsbury G;  
XX  
DR WPI; 2003-058477/05.  
XX  
PT Novel substantially purified antibody immunospecifically binding to TANGO  
PT 268 antigen, useful for treating bleeding disorders such as  
PT thrombocytopenia, stroke, ischemia, pulmonary embolism, atherosclerosis.  
XX  
PS Disclosure; Page 212; 236pp; English.  
XX  
CC This invention relates to a novel purified antibody comprising a variable  
CC heavy (VH) complementarity determining region (CDR)1, VH CDR2 or VH CDR3;  
CC or variable light (VL) CDR1, VL CDR2 or VL CDR3, and immunospecifically  
CC binding to a TANGO 268 (also referred as glycoprotein VI (GPVI)) antigen.  
CC The antibodies of the invention act to decrease or block TANGO 268  
CC binding to extracellular matrix components, or as a Collagen or platelet  
CC release and aggregation blocker. The antibodies of the invention are  
CC useful for modulating proliferation, migration, morphology,  
CC differentiation and/or function of megakaryocytes and platelets,  
CC including during development e.g. embryogenesis, modulating leukocyte-  
CC platelet and platelet-endothelium interactions in inflammation and/or  
CC thrombosis, and modulating platelet aggregation and degranulation. They  
CC are also useful for modulating disorders associated with abnormal or  
CC aberrant megakaryocyte and/or platelet proliferation, migration,  
CC morphology, differentiation and/or function, e.g. bleeding disorders such  
CC as thrombocytopenia. Other diseases which may be modulated by these  
CC antibodies are thrombotic disorders, cerebral vascular diseases (e.g.  
CC stroke and ischaemia) venous thromboembolism diseases (e.g. diseases  
CC involving leg swelling, pain and ulceration, pulmonary embolism, etc);  
CC coronary diseases (e.g. cardiovascular diseases including angina  
CC pectoris, myocardial infarction, coronary restenosis, atherosclerosis,  
CC etc); immunological disorders, developmental disorders, embryonic  
CC disorders, liver disorders, cerebral vascular diseases, venous  
CC thromboembolism disease, coronary diseases, and metastatic cancers. The

CC antibodies of the invention only causes a transient decrease in platelet  
CC counts, platelet aggregation, and/or platelet activation and so have some  
CC advantages over prior art methods. The present sequence represents a  
CC peptide sequence used to generate the antibodies of the invention  
XX  
SQ

Sequence 47 AA;  
Query Match 100.0%; Score 268; DB 6; Length 47;  
Best Local Similarity 100.0%; Pred. No. 2.5e-28;  
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 COTRYGDPQALYKGGDPAPYKNPERWYRASFPFIITVTAHSGTYRC 47  
Db 1 COTRYGDPQALYKGGDPAPYKNPERWYRASFPFIITVTAHSGTYRC 47

RESULT 3  
AAB61272  
ID AAB61272 standard; protein; 47 AA.

AC AAB61272;  
DT 04-APR-2001 (first entry)  
XX Mouse TANGO 268 Ig-like domain #2.

DE Mouse; TANGO 268; cardiant; cerebroprotective; cytostatic; anticoagulant;  
KW thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI;  
KW platelet membrane glycoprotein receptor; bleeding disorder;  
KW blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;  
KW ischaemia; cardiovascular disease; immunological disease; liver disorder;  
KW cancer.

OS Mus musculus.  
XX WO200100810-A1.

PN 04-JAN-2001.  
PD 30-JUN-2000; 2000WO-US018152.

PF 30-JUN-1999; 99US-00345468.  
PR 06-DEC-1999; 99US-00454824.  
PR 14-FEB-2000; 2000US-00503387.

XX (MILL-) MILLENNIUM PHARM INC.  
XX Busfield SJ, Villel J, Jandrot-Perrus M, Vainchencker W;  
PI Gill DS, Qian MD, Kingsbury G;  
XX WPI; 2001-080877/09.

DR New genes encoding human platelet-expressed collagen receptor,  
XX glycoprotein VI, and its modulators, useful for preventing, treating and  
XX diagnosing hemorrhagic disorders, thrombotic diseases and immunological  
XX disorders.

PS Disclosure; Page 210-211; 227pp; English.

XX The present sequence is given in a specification relating to an isolated  
XX nucleic acid molecule encoding a platelet membrane glycoprotein receptor  
XX glycoprotein VI (GPVI), also called TANGO 268. The GPVI polynucleotides  
XX and polypeptides and their modulators, e.g. antisense nucleic acids,  
XX ribozymes and antibodies, are useful for preventing, treating and  
XX diagnosing disorders associated with aberrant expression or activity of  
XX GPVI. These disorders include bleeding disorders (e.g.  
XX thrombocytopenia), blood vessel injury, thrombotic disorders (e.g.  
XX thrombotic occlusion of the coronary arteries), haemorrhagic disorders,  
XX coronary artery and cerebral artery diseases (e.g. stroke and ischaemia),  
XX cardiovascular diseases (e.g. atherosclerosis and myocardial infarction),  
XX immunological diseases (e.g. platelet disorder) and embryonic liver  
XX disorders. Preferably they are used to prevent acute cardiac ischaemia  
XX following angioplasty and metastatic cancers, especially of the colon and

CC liver  
XX  
SQ

Sequence 47 AA;  
Query Match 82.1%; Score 220; DB 4; Length 47;  
Best Local Similarity 78.7%; Pred. No. 7.2e-22;  
Matches 37; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 COTRYGDPQALYKGGDPAPYKNPERWYRASFPFIITVTAHSGTYRC 47  
Db 1 CQSPYSDFEFLYKGGTGYKPKPKWYRANFPIITVTAHSGTYRC 47

RESULT 4  
ABU11238  
ID ABU11238 standard; peptide; 47 AA.

AC ABU11238;  
DT 06-FEB-2003 (first entry)  
XX TANGO 268 IgG like domain #2.

DE Human; mouse; variable heavy; VH; antigen; cancer;  
KW complementarity determining region; TANGO 268; glycoprotein VI; GPVI;  
KW TANGO 268; extracellular matrix; collagen; inflammation; thrombosis;  
KW proliferation; migration; embryogenesis; antibody; thrombotic disorder;  
KW degeneration; thrombocytopenia; stroke; ischaemia; venous thromboembolism;  
KW cerebral vascular disease; angina pectoris; myocardial infarction;  
KW leg swelling; pain; ulceration; pulmonary embolism; coronary disease;  
KW cardiovascular disease; atherosclerosis; immunological disorder;  
KW coronary restenosis; embryonic disorder; liver disorder;  
KW developmental disorder; venous thromboembolism disease.  
KW cerebral vascular disease; venous thromboembolism disease.

OS Mus musculus.  
XX WO200280968-A1.

PN 17-OCT-2002.  
PD 09-APR-2002; 2002WO-US011122.

PF 09-APR-2001; 2001US-00829495.  
PR (MILL-) MILLENNIUM PHARM INC.

XX Busfield SJ, Villel J, Jandrot-Perrus M, Vainchencker W;  
PI Gill DS, Qian DM, Kingsbury G;  
XX WPI; 2003-058477/05.

DR Novel substantially purified antibody immunospecifically binding to TANGO  
XX 268 antigen, useful for treating bleeding disorders such as  
XX thrombocytopenia, stroke, ischemia, pulmonary embolism, atherosclerosis.

PS Disclosure; Page 219; 236pp; English.

XX This invention relates to a novel purified antibody comprising a variable  
XX heavy (VH) complementarity determining region (CDR)1, VH CDR2 or VH CDR3;  
XX or variable light (VL) CDR1, VL CDR2 or VL CDR3, and immunospecifically  
XX binding to a TANGO 268 (also referred as glycoprotein VI (GPVI)) antigen.  
XX The antibodies of the invention act to decrease or block TANGO 268  
XX binding to extracellular matrix components, or as a Collagen or platelet  
XX release and aggregation blocker. The antibodies of the invention are  
XX useful for modulating proliferation, migration, morphology,  
XX differentiation and/or function of megakaryocytes and platelets,  
XX including during development e.g. embryogenesis, modulating leukocyte-  
XX platelet and platelet-endothelium interactions in inflammation and/or  
XX thrombosis, and modulating platelet aggregation and degradation. They  
XX are also useful for modulating disorders associated with abnormal or  
XX aberrant megakaryocyte and/or platelet proliferation, migration,  
XX morphology, differentiation and/or function, e.g. bleeding disorders such

as thrombocytopaenia. Other diseases which may be modulated by these antibodies are thrombotic disorders, cerebral vascular diseases (e.g. stroke and ischaemia) venous thromboembolism diseases (e.g. diseases involving leg swelling, pain and ulceration, pulmonary embolism, etc); coronary diseases (e.g. cardiovascular diseases including angina pectoris, myocardial infarction, coronary stenosis, atherosclerosis, etc); immunological disorders, developmental disorders, venous disorders, liver disorders, cerebral vascular diseases, embolic thromboembolism disease, coronary diseases, and metastatic cancers. The antibodies of the invention only causes a transient decrease in platelet counts, platelet aggregation, and/or platelet activation and so have some advantages over prior art methods. The present sequence represents a peptide sequence used to generate the antibodies of the invention

Query Match	82.1%	Score 220;	DB 6;	Length 47;
Best Local Similarity	78.7%;	Pred. No. 7.2e-22;		
Matches 37;	Conservative 4;	Mismatches 6;	Indels 0;	Gaps 0;

RESULT 5	
AAB19610	
ID	AAB19610 standard; peptide; 42 AA.
XX	
XX	
AC	AAB19610;
XX	
DT	22-JAN-2001 (first entry)
XX	
DE	Glucagon-like peptide 1 receptor N-terminal domain peptide 2.
XX	
KW	Glucagon-like peptide 1; G-coupled protein receptor; GLP-1R; vaccine;
KW	metabolic disease; nervous system disorder;
KW	extramembranous receptor domain; ERD; cancer.

Chemically synthesised peptide 2 is 1 of 3 peptides (see also AAB19609 and AAB19611) used in the preparation of the N-terminal domain (see AAB19612) of glucagon-like peptide 1 receptor in an example of the method of the invention. This relates to the chemical synthesis of extramembranous receptor domains (ERDs), such as the soluble ligand-binding extracellular and cytosolic domains, of membrane protein receptors. The ERDs are produced by ligating, under chemoselective ligation conditions, first and second peptides of an ERD of a membrane protein receptor, where the peptides have unprotected chemoselective reactive groups capable of forming a covalent bond. The ligation product is exposed to a folding buffer having a chaotropic reagent and an organic

solvent that approximates the water-lipid interface of a cell membrane. Exposure to the folding buffer is followed by isolation from the buffer of ligation product that binds to a ligand of the membrane protein receptor. The ligand-binding portion of the ligation product represents folded ERD. The invention is exemplified by total chemical synthesis of the N-terminal domain of glucagon-like peptide 1 receptor, demonstration of its ability to bind to peptide ligand and characterization of its disulphide map. The method provides access to non-limiting amounts of ultra-pure and ultra-homogeneous soluble ERDs useful for drug discovery, high-throughput screening of receptor ligands, as therapeutics, e.g. for treatment of metabolic diseases, nervous system diseases and cancer, and as vaccines

SQ Sequence 42 AA;  
 Query Match 17.7%; Score 47.5; DB 3; Length 42;  
 Best Local Similarity 34.8%; Pred. No. 97;  
 Matches 8; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

RESULT 6	
ADM34378	
ID	ADM34378 standard; peptide; 34 AA.
XX	
AC	ADM34378;
XX	
DT	03-JUN-2004 (first entry)
XX	
DE	Human IY1448P cancer related peptide for cancer detection method.
XX	
KW	cytostatic; T-cell vaccine; detection; cancer;
KW	chronic lymphocytic leukemia.
XX	
OS	Homo sapiens.
XX	
PN	WO2003077836-A2.
XX	
PD	25-SEP-2003.
XX	
PF	06-NOV-2002; 2002WO-US035728.
XX	
PR	06-NOV-2001; 2001US-00040862.
PR	23-MAY-2002; 2002US-00154884.
XX	
PA	(CORI-) CORIXA CORP.
XX	
PI	Gaiger A, Algate PA, Mannion J, Retter M;
XX	
DR	WPI; 2003-756941/71.

The invention relates to a method of detecting (M1) cancer in a patient by: (i) contacting a biological sample from the patient with an agent that binds to any of three polypeptides given in the specification; (ii) detecting in a sample an amount of the peptide that binds to the binding agent; and (iii) comparing the amount of polypeptide present in the patient's sample to a predetermined cutoff value. The specification also discloses a separate method for detecting (M2) cancer in a patient by a method similar to M1, except that the detection agent is an oligonucleotide that binds to any of three polynucleotides given in the specification. M1 and M2 are useful for detecting the presence of cancer in a patient, especially chronic lymphocytic leukemia. The applicants have identified specific human polypeptides overexpressed in one or more

CC types of hematological malignancies. This sequence corresponds to a  
CC peptide used in the method of the invention.  
XX  
SQ Sequence 34 AA;  
Query Match 17.4%; Score 46.5; DB 7; Length 34;  
Best Local Similarity 55.6%; Pred. No. 1e+02;  
Matches 10; Conservative 3; Mismatches 4; Indels 1; Gaps 1;  
QY 30 ASPPIITVTAHSGTYRC 47  
DB 12 ASFN-LSLTAHSGNYSC 28  
RESULT 7  
AAY20266  
ID AAY20266 standard; protein; 38 AA.  
XX  
AC AAY20266;  
XX  
DT 22-JUL-1999 (first entry)  
DE Human ubiquitin B mutant protein fragment 5.  
XX  
KW Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;  
KW frameshift mutation; age-related disease; neurodegenerative disorder;  
KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;  
KW Huntington's disease; multiple sclerosis; alcoholic liver disease;  
KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;  
KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;  
KW neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;  
KW glial fibrillary acidic protein; GFAP; p53; senaphorin III; HUPF-1;  
KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;  
KW high mobility group protein-C; neuroendocrine specific protein A.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
XX WO9845322-A2.  
XX  
PD 15-OCT-1998.  
XX  
PF 02-APR-1998; 98WO-IB000705.  
XX  
PR 10-APR-1997; 97US-0043163P.  
XX  
PA (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.  
PA (UYRO-) UNIV ROTTERDAM ERASMUS.  
PA (UYUT-) RIJKSUNIV UTRECHT.  
XX  
PI Van Leeuwen FW, Grosveld FG, Burbach JPH;  
DR WPI; 1998-609901/51.  
DR N-PSDB; AAX75755.  
XX  
XX Diagnosing disease by detecting frameshift mutations in RNA or  
PT corresponding protein mutations - used to diagnose cancer and  
PT neurological diseases, particularly Alzheimer's disease, and also for  
PT treatment and prevention with specific ribozymes or wild-type RNA.  
XX  
PS Disclosure; Fig 4; 258pp; English.  
XX  
XX This invention describes a novel method for the diagnosis of a disease  
CC caused by, or associated with, an RNA molecule that has a frameshift  
CC mutation. The method is used to diagnose age-related diseases, especially  
CC cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's  
CC disease, Down's syndrome, myotonic dystrophy, Huntington's disease,  
CC multiple sclerosis, alcoholic liver disease, diabetes mellitus type II  
CC and many others listed) or susceptibility to these disorders. The method  
CC allows a definitive diagnosis of Alzheimer's disease in living patients,  
CC at an early stage. It is based on the observation that disease may be  
CC caused by mutations in RNA rather than DNA. The invention describes the  
CC use of neuronal system RNA molecules, specifically proteins including

CC beta-amyloid precursor protein (beta-APP), the microtubule associated  
CC proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule  
CC associated protein 2 (MAP2), neurofilament-L, neurofilament-M,  
CC neurofilament-F, presenilin I, presenilin II, glial fibrillary acidic  
CC protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma  
CC 2 (bcl-2) proto-oncogene, senaphorin III, HUPF-1, high mobility group  
CC protein-C (HMGP-C) and neuroendocrine specific protein A  
XX  
SQ Sequence 38 AA;  
Query Match 17.4%; Score 46.5; DB 2; Length 38;  
Best Local Similarity 58.8%; Pred. No. 1.2e+02;  
Matches 10; Conservative 1; Mismatches 5; Indels 1; Gaps 1;  
QY 13 YKEG-DPAPYKNPERWY 28  
DB 3 HPEGVDPAFGPASRWY 19  
RESULT 8  
AAY20269  
ID AAY20269 standard; protein; 38 AA.  
XX  
AC AAY20269;  
XX  
DT 22-JUL-1999 (first entry)  
DE Human ubiquitin B mutant protein fragment 8.  
XX  
KW Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;  
KW frameshift mutation; age-related disease; neurodegenerative disorder;  
KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;  
KW Huntington's disease; multiple sclerosis; alcoholic liver disease;  
KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;  
KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;  
KW neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;  
KW glial fibrillary acidic protein; GFAP; p53; senaphorin III; HUPF-1;  
KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;  
KW high mobility group protein-C; neuroendocrine specific protein A.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
XX WO9845322-A2.  
XX  
PD 15-OCT-1998.  
XX  
PF 02-APR-1998; 98WO-IB000705.  
XX  
PR 10-APR-1997; 97US-0043163P.  
XX  
PA (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.  
PA (UYRO-) UNIV ROTTERDAM ERASMUS.  
PA (UYUT-) RIJKSUNIV UTRECHT.  
XX  
PI Van Leeuwen FW, Grosveld FG, Burbach JPH;  
DR WPI; 1998-609901/51.  
DR N-PSDB; AAX75755.  
XX  
XX Diagnosing disease by detecting frameshift mutations in RNA or  
PT corresponding protein mutations - used to diagnose cancer and  
PT neurological diseases, particularly Alzheimer's disease, and also for  
PT treatment and prevention with specific ribozymes or wild-type RNA.  
XX  
PS Disclosure; Fig 4; 258pp; English.  
XX  
XX This invention describes a novel method for the diagnosis of a disease  
CC caused by, or associated with, an RNA molecule that has a frameshift  
CC mutation. The method is used to diagnose age-related diseases, especially  
CC cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's  
CC disease, Down's syndrome, myotonic dystrophy, Huntington's disease,  
CC multiple sclerosis, alcoholic liver disease, diabetes mellitus type II  
CC and many others listed) or susceptibility to these disorders. The method  
CC allows a definitive diagnosis of Alzheimer's disease in living patients,  
CC at an early stage. It is based on the observation that disease may be  
CC caused by mutations in RNA rather than DNA. The invention describes the  
CC use of neuronal system RNA molecules, specifically proteins including

CC and many others listed) or susceptibility to these disorders. The method  
 CC allows a definitive diagnosis of Alzheimer's disease in living patients,  
 CC at an early stage. It is based on the observation that disease may be  
 CC caused by mutations in RNA rather than DNA. The invention describes the  
 CC use of neuronal system RNA molecules, specifically proteins including  
 CC beta-amyloid precursor protein (beta-ApP), the microtubule associated  
 CC proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule  
 CC associated protein 2 (MAP2), neurofilament-L, neurofilament-M,  
 CC neurofilament-F, presenilin 1, presenilin 2, glial fibrillary acidic  
 CC protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma  
 CC 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group  
 CC protein-C (HMGPC) and neuroendocrine specific protein A

XX SQ Sequence 38 AA;

Query Match 17.4%; Score 46.5; DB 2; Length 38;  
 Best Local Similarity 58.8%; Pred. No. 1.2e+02;  
 Matches 10; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

Qy 13 YKEG-DPAPYKNPRRWY 28  
 : || ||||| |||||  
 Db 3 HPEGVDPAFGPASERWY 19

RESULT 9  
 ABR83767  
 ID ABR83767 standard; peptide: 44 AA.

XX AC ABR83767;

XX DT 15-OCT-2003 (first entry)

XX DE Pseudomonas putida nlpD protein amino acids 44-87.

XX KW Antibacterial; protozoacide; vaccine; cell-wall material; anchor protein;  
 KW Gram-positive bacterium; Lactococcus lactis; Acma; biocatalyst;  
 KW mucosal immunization; biosorbent; biofilter; microbiocatalyst;  
 KW vaccination; malaria; Streptococcus pneumoniae; fusion gene;  
 KW Streptococcus pneumoniae; protease maturation protein.

XX OS Pseudomonas putida.

XX PN WO2002101026-A2.

XX PD 19-DEC-2002.

XX PF 11-JUN-2002; 2002WO-NL000383.

XX PR 11-JUN-2001; 2001EP-0020239.

XX PA (NANO-) APPLIED NANOSYSTEMS BV.

XX PI Leenhouts CJ, Ramaesamy R, Steen A, Kok J, Buist G, Kuipers OP;

XX DR WPI; 2003-167404/16.

XX PT Improving binding of a proteinaceous substance e.g. an Acma-type protein  
 to a cell-wall material of microorganisms, comprises treating the  
 PT material with a solution capable of removing protein or carbohydrate from  
 PT the material.

XX FS Example 3; Fig 24; 77pp; English.

XX CC The invention relates to a method of obtaining cell-wall material of a  
 CC Gram-positive bacterium with improved capacity for binding to a  
 CC proteinaceous substance (PS), or binding PS to cell-wall material of the  
 CC bacterium, by treating the cell-wall material with a solution capable of  
 CC removing a cell-wall component such as a protein, (lipo)teichoic acid or  
 CC carbohydrate from the material. The method especially uses the binding of  
 CC the PS with an anchor protein from the cell wall of the organism. The  
 CC anchor protein is preferably the Lactococcus lactis Acma cell wall  
 CC binding domain or its homolog or functional derivative. The method is  
 CC useful for improving binding of proteinaceous substance to cell wall

CC material of gram-positive bacterium, e.g. for the preparation of a  
 CC pharmaceutical composition comprising a vaccine useful for mucosal  
 CC immunization and for preparing a biocatalyst. The preparation is also  
 CC useful for generating bioadsorbents or biofilters for environmental  
 CC purposes, microbiocatalysts and diagnostic tools. Also for vaccination  
 CC purposes, to elicit immunity for pathogens, like malaria and  
 CC Streptococcus pneumoniae. In an example of the invention, acid  
 CC pretreatment of Gram-positive bacteria to enhance binding of Acma protein  
 CC anchor fusion is investigated by the construction of a reporter plasmid  
 CC encoding a fusion gene of the L. lactis Acma protein and the  
 CC Streptococcus pneumoniae protease maturation protein PpmA. This sequence  
 CC represents a homologue of the Lactococcus lactis Acma anchor protein. The  
 CC region can be used in the generation of the fusion protein of the  
 CC invention

XX SQ Sequence 44 AA;

Query Match 17.0%; Score 45.5; DB 6; Length 44;  
 Best Local Similarity 52.2%; Pred. No. 1.9e+02;  
 Matches 12; Conservative 1; Mismatches 1; Indels 9; Gaps 2;

Qy 4 RYGFDFQFALYKE-----GDPAPY 21  
 |||:| ||| | ||||  
 Db 15 RYGWD----YKELAARNGIPAPY 33

RESULT 10

ADF70087

ID ADF70087 standard; protein; 44 AA.

XX AC ADF70087;

XX DT 12-FEB-2004 (first entry)

XX DE Acma-type homologue amino acid sequence.

XX KW delivery; targeting system; Acma-type anchor protein; solid tumour;  
 KW health; medical; agricultural; cosmetic; controlled release.

XX OS Pseudomonas putida.

XX PN WO2003084508-A1.

XX PD 16-OCT-2003.

XX PF 04-APR-2003; 2003WO-NL000256.

XX PR 04-APR-2002; 2002EP-00076316.

XX PR 04-APR-2002; 2002US-0369927P.

XX PR 05-APR-2002; 2002US-0370485P.

XX PR 20-DEC-2002; 2002EP-00080481.

XX PA (NANO-) APPLIED NANOSYSTEMS BV.

XX PI Friesen RHE, Leenhouts CJ, Hektor HJ, Van Esch JH, Heeres A;

XX PI Robillard GT;

XX DR WPI; 2003-877005/81.

XX PT Vehicle for targeted delivery of therapeutic or diagnostic agents,  
 PT includes protein anchor and system for inducing availability of the  
 PT agent.

XX FS Example 3; Page 196; 303pp; English.

XX CC The present invention describes a vehicle (A) for delivering a substance  
 CC (I) to a predetermined site, which comprises (I); a system for inducing  
 CC availability of at least one compartment of (A) towards the exterior;  
 CC and, as targeting system for directing (A) to the site, an Acma-type  
 CC anchor protein (II). (A) are used for delivery of diagnostic and  
 CC therapeutic agents to predetermined sites in the body, particularly  
 CC joints or solid tumours but can be used more generally for health,  
 CC medical, agricultural and cosmetic applications. (A) significantly

CC increases the half-life of peptides in the circulation and, by providing  
CC controlled release, ensures relatively high bioavailability, allowing  
CC therapeutic use of agents that would otherwise be too toxic for systemic  
CC administration. The native Acma peptide targets Gram-positive bacteria  
CC but its homologues can be engineered to have different selectivity. The  
CC present sequence is used in the exemplification of the present invention.

XX Sequence 44 AA;

Query Match 17.0%; Score 45.5; DB 7; Length 44;  
Best Local Similarity 52.2%; Pred. No. 1.9e+02;  
Matches 12; Conservative 1; Mismatches 1; Indels 9; Gaps 2;

QY 4 RYGFDPALYKE-----GDPAPY 21  
DB 15 RYGD-----YKELAAANGIPAPY 33

RESULT 11

AB99764  
ID ABB99764 standard; peptide; 24 AA.

XX

AC ABB99764;

DT 24-MAR-2003 (first entry)

XX Antigenic peptide derived from CD200 receptor isoform CD200R1.

XX Mouse; cluster of differentiation 200 receptor; CD200 receptor; isoform;  
KW CD200R2a; CD200b; CD200a; immune response; graft rejection; diabetes;  
KW foetal loss; autoimmunity; allergy; inflammatory condition; cancer;  
KW skin condition; transplant rejection; autoimmune disease; arthritis;  
KW immune suppression; infection.

XX Synthetic.

OS Mus musculus.

PN WO200295030-A2.

XX

PD 28-NOV-2002.

XX 24-MAY-2002; 2002WO-CA000734.

XX 24-MAY-2001; 2001US-0292950P.

PR 05-APR-2002; 2002US-0369862P.

XX (TRAN-) TRANSPLANTATION TECHNOLOGIES INC.

PI Gorczynski RM, Marsden P;

XX WPI; 2003-148469/14.

XX New cluster of differentiation 200 receptor (CD200R)2a, CD200R2b, and  
PT CD200R3a proteins, for manufacturing a medicament to modulate an immune  
PT response involved in e.g. graft rejection, autoimmunity, or allergy.

XX Example 2; Page 60; 189pp; English.

XX Peptides ABB9764-69 represents antigenic peptides derived from cluster  
CC of differentiation 200 (CD200) receptor isoforms. The peptides were used  
CC to raise antibodies. The CD200 receptor is present in isoforms CD200R2a,  
CC CD200R2b and CD200R3a. The CD200R2a, CD200R2b, and CD200R3a proteins,  
CC nucleic acids, or antibodies against the proteins are useful for  
CC manufacturing a medicament to modulate an immune response involved in  
CC graft rejection, fetal loss, autoimmunity, allergy, inflammatory  
CC conditions, skin conditions, or cancer. CD200 receptor agonists or a  
CC population of suppressive antigen presenting cells or T cells or its  
CC precursors are useful for manufacturing a medicament to suppress an  
CC immune response. The agonists are useful for preventing or treating  
CC transplant rejection, fetal loss, allergy, inflammatory conditions, skin  
CC conditions, or autoimmune disease, such as arthritis or diabetes. A CD200  
CC receptor antagonist is useful for manufacturing a medicament to inhibit  
CC immune suppression. The antagonists are useful for preventing or treating

CC cancer, or viral, bacterial or fungal infections  
XX Sequence 24 AA;

Query Match 16.8%; Score 45; DB 6; Length 24;  
Best Local Similarity 39.3%; Pred. No. 1e+02;  
Matches 11; Conservative 1; Mismatches 10; Indels 6; Gaps 1;

QY 20 PYKPERMYRASFPITVTAAHSGTYRC 47  
DB 3 PDHSPE-----LOISAVTLQHEGYTC 24

RESULT 12

ADM35220  
ID ADM35220 standard; peptide; 30 AA.

XX

AC ADM35220;

DT 03-JUN-2004 (first entry)

XX Human LY1448P cancer related peptide for cancer detection method.  
DE cytostatic; T-cell vaccine; detection; cancer;  
XX chronic lymphocytic leukemia.

XX Homo sapiens.

XX WO2003077836-A2.

XX 25-SEP-2003.

XX 06-NOV-2002; 2002WO-US035728.

XX 06-NOV-2001; 2001US-00040862.

XX 23-MAY-2002; 2002US-00154884.

XX (CORI-) CORIXA CORP.

XX Gaiger A, Algate PA, Mannion J, Retter M;

XX WPI; 2003-756941/71.

XX Detecting cancer in a patient comprises contacting a biological sample  
PT from the patient with a binding agent that binds to a cancer-associated  
PT polypeptide and comparing the amount of polypeptide to a predetermined  
PT cutoff value.

XX Disclosure; SEQ ID NO 10445; 419pp; English.

XX The invention relates to a method of detecting (M1) cancer in a patient  
CC by: (i) contacting a biological sample from the patient with an agent  
CC that binds to any of three polypeptides given in the specification; (ii)  
CC detecting in a sample an amount of the peptide that binds to the binding  
CC agent; and (iii) comparing the amount of polypeptide present in the  
CC patient's sample to a predetermined cutoff value. The specification also  
CC discloses a separate method for detecting (M2) cancer in a patient by a  
CC method similar to M1, except that the detection agent is an  
CC oligonucleotide that binds to any of three polynucleotides given in the  
CC specification. M1 and M2 are useful for detecting the presence of cancer  
CC in a patient, especially chronic lymphocytic leukemia. The applicants  
CC have identified specific human polypeptides overexpressed in one or more  
CC types of hematological malignancies. This sequence corresponds to a  
CC peptide used in the method of the invention.

XX Sequence 30 AA;

Query Match 16.8%; Score 45; DB 7; Length 30;  
Best Local Similarity 53.8%; Pred. No. 1.4e+02;  
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 35 ITVTAHSGTYRC 47  
DB 3 ITVTAHSGTYRC 47

Db	4 LSLTAHSGNSYC 16	XX	Human cardiovascular system antigen polypeptide SEQ ID No 997.
RESULT 13		DE	
ADM35348		XX	Cardiovascular system antigen; human; mouse; rabbit; goat; horse; cat;
ID	ADM35348 standard; peptide; 41 AA.	KW	chicken; sheep; immunosuppressive; antiarthritic; vasotropic; dog;
XX		KW	antirheumatic; antiproliferative; cytostatic; cardiac; neuroprotective;
AC	ADM35348;	KW	cerebroprotective; nootropic; antibacterial; viricide; fungicide; cancer;
XX		KW	ophthalmological; vulnary; gene therapy; autoimmune disease; neoplasm;
DT	03-JUN-2004 (first entry)	KW	hyperproliferative disorder; breast; liver; cardiovascular disorder;
XX		KW	cerebrovascular disorder; nervous system disorder; bacterial infection;
DE	Human LY1448P cancer related peptide for cancer detection method.	KW	fungal infection; viral infection; ocular disorder; endocrine disorder;
XX		KW	gastrointestinal disorder; renal disorder; respiratory disorder;
KW	cytostatic; T-cell vaccine; detection; cancer;	KW	wound healing; skin aging; organ transplantation; tissue regeneration;
KW	chronic lymphocytic leukemia.	XX	anti-infertility.
OS	Homo sapiens.	XX	
XX		OS	Homo sapiens.
XX		PN	WO200155321-A2.
PN	WO2003077836-A2.	XX	
XX		XX	02-AUG-2001.
PD	25-SEP-2003.	PD	
XX		XX	17-JAN-2001; 2001WO-US001340.
PF	06-NOV-2002; 2002WO-US035728.	XX	
XX		PR	31-JAN-2000; 2000US-0179065P.
XX		PR	04-FEB-2000; 2000US-0180628P.
PR	06-NOV-2001; 2001US-00040862.	PR	24-FEB-2000; 2000US-0184664P.
PR	23-MAY-2002; 2002US-00154884.	PR	02-MAR-2000; 2000US-0186350P.
XX		PR	16-MAR-2000; 2000US-0189874P.
PA	(CORI-) CORIXA CORP.	PR	17-MAR-2000; 2000US-0190076P.
XX		PR	18-APR-2000; 2000US-0198123P.
PI	Gaiger A, Algate PA, Mannion J, Retter M;	PR	19-MAY-2000; 2000US-0205515P.
XX		PR	07-JUN-2000; 2000US-0209467P.
DR	WPI; 2003-756941/71.	PR	28-JUN-2000; 2000US-0214886P.
XX		PR	30-JUN-2000; 2000US-0215135P.
PT	Detecting cancer in a patient comprises contacting a biological sample	PR	07-JUL-2000; 2000US-0216647P.
PT	from the patient with a binding agent that binds to a cancer-associated	PR	11-JUL-2000; 2000US-0216880P.
PT	polypeptide and comparing the amount of polypeptide to a predetermined	PR	11-JUL-2000; 2000US-0217487P.
XX	cutoff value.	PR	11-JUL-2000; 2000US-0217496P.
XX		PR	14-JUL-2000; 2000US-0218290P.
PS	Disclosure; SEQ ID NO 11154; 419pp; English.	PR	26-JUL-2000; 2000US-0220963P.
XX		PR	26-JUL-2000; 2000US-0220964P.
CC	The invention relates to a method of detecting (M1) cancer in a patient	PR	14-AUG-2000; 2000US-0224518P.
CC	by: (i) contacting a biological sample from the patient with an agent	PR	14-AUG-2000; 2000US-0224519P.
CC	that binds to any of three polypeptides given in the specification; (ii)	PR	14-AUG-2000; 2000US-0225213P.
CC	detecting in a sample an amount of the peptide that binds to the binding	PR	14-AUG-2000; 2000US-0225214P.
CC	agent; and (iii) comparing the amount of polypeptide present in the	PR	14-AUG-2000; 2000US-0225266P.
CC	patient's sample to a predetermined cutoff value. The specification also	PR	14-AUG-2000; 2000US-0225267P.
CC	discloses a separate method for detecting (M2) cancer in a patient by a	PR	14-AUG-2000; 2000US-0225268P.
CC	method similar to M1, except that the detection agent is an	PR	14-AUG-2000; 2000US-0225270P.
CC	oligonucleotide that binds to any of three polynucleotides given in the	PR	14-AUG-2000; 2000US-0225447P.
CC	specification. M1 and M2 are useful for detecting the presence of cancer	PR	14-AUG-2000; 2000US-0225757P.
CC	in a patient, especially chronic lymphocytic leukemia. The applicants	PR	14-AUG-2000; 2000US-0225758P.
CC	have identified specific human polypeptides overexpressed in one or more	PR	14-AUG-2000; 2000US-0225759P.
CC	types of hematological malignancies. This sequence corresponds to a	PR	18-AUG-2000; 2000US-0226279P.
CC	peptide used in the method of the invention.	PR	22-AUG-2000; 2000US-0226681P.
XX		PR	22-AUG-2000; 2000US-0226686P.
SQ	Sequence 41 AA;	PR	22-AUG-2000; 2000US-0227182P.
		PR	23-AUG-2000; 2000US-0227009P.
	Query Match 16.8%; Score 45; DB 7; Length 41;	PR	30-AUG-2000; 2000US-0228924P.
	Best Local Similarity 53.8%; Pred. No. 2e+02;	PR	01-SEP-2000; 2000US-0229287P.
	Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;	PR	01-SEP-2000; 2000US-0229343P.
QY	35 ITVTAHSGTYRC 47	PR	01-SEP-2000; 2000US-0229344P.
	:::	PR	01-SEP-2000; 2000US-0229345P.
Db	3 LSLTAHSGNSYC 15	PR	05-SEP-2000; 2000US-0229509P.
		PR	05-SEP-2000; 2000US-0229513P.
RESULT 14		PR	06-SEP-2000; 2000US-0230437P.
AAU22223		PR	06-SEP-2000; 2000US-0230438P.
ID	AAU22223 standard; protein; 45 AA.	PR	08-SEP-2000; 2000US-0231242P.
XX		PR	08-SEP-2000; 2000US-0231243P.
AC	AAU22223;	PR	08-SEP-2000; 2000US-0231244P.
XX		PR	08-SEP-2000; 2000US-0231413P.
DT	18-DEC-2001 (first entry)	PR	08-SEP-2000; 2000US-0231414P.
		PR	08-SEP-2000; 2000US-0232080P.



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PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-02323063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241828P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249246P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249279P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.

PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-451930/48.
XX N-PSDB; AAS35497.
XX New cardiovascular system related polynucleotides and polypeptides,
XX useful for diagnosing, treating and/or preventing disorders of the
XX cardiovascular system.
XX Claim 11; SEQ ID NO 997; 674bp; English.
XX Sequences AU21852-AU22466 represent the cardiovascular system antigen
XX polypeptides of the invention. Cardiovascular system antigens and their
XX associated polynucleotides are useful in the diagnosis, treatment and
XX prevention of various types of disorders in e.g. humans, mice, rabbits,
XX goats, horses, cats, dogs, chickens or sheep. A pathological condition
XX can be determined by detecting the presence or absence of a mutation in a
XX cardiovascular system antigen polynucleotide. The treatable disorders
XX include autoimmune diseases such as rheumatoid arthritis,
XX hyperproliferative disorders such as cardiac arrest, cerebrovascular
XX disorders such as cerebral ischaemia, nervous system disorders such as
XX Alzheimer's disease, infections caused by bacteria, viruses and fungi,
XX ocular disorders such as corneal infection, endocrine disorders such as
XX premature labour and infertility, gastrointestinal disorders such as
XX Crohn's disease, renal disorders such as asthma and pleurisy. The polypeptides can
XX respiratory disorders such as asthma and pleurisy. The polypeptides can
XX also be used to aid wound healing, to prevent skin aging due to sunburn,
XX to maintain organs before transplantation, to regenerate tissues and in
XX chemotaxis. Note: The sequence data for this patent did not form part of
XX the printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences

Query Match 16.6%; Score 44.5; DB 4; Length 45;
Best Local Similarity 38.5%; Pred. NO. 2.7e+02;
Matches 15; Conservative 1; Mismatches 12; Indels 11; Gaps 2;

QY 9 QPALLYKEGDPAKYKNPERWYRASPFIITVTAHSGTYRC 47
DB 1 QFLLDKLG-----MTASIPLI--TGVHSGKRC 28

RESULT 15
ADE46191
ID ADE46191 standard; protein; 45 AA.
XX
AC ADE46191;
XX
XX 29-JAN-2004 (first entry)
XX
XX Human cardiovascular system related polypeptide #372.
XX
XX Human; cardiovascular system related polypeptide; cancer;
XX proliferative disorder; foetal abnormality; developmental abnormality;
XX haematopoietic disorder; AIDS; autoimmune disease; rheumatoid arthritis;
XX inflammation; allergy; neurological disorder; Alzheimer's disease;
XX
```

KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;  
KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;  
KW cardiovascular disorder; angiogenic disorder; kidney disorder;  
KW gastrointestinal disorder; pregnancy-related disorder;  
endocrine disorder.

XX OS  
XX Homo sapiens.

PN US2003059908-A1.

XX 27-MAR-2003.

XX 07-MAR-2002; 2002US-00091504.

XX 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184664P.

PR 02-MAR-2000; 2000US-0186350P.

PR 16-MAR-2000; 2000US-0189874P.

PR 17-MAR-2000; 2000US-0190076P.

PR 18-APR-2000; 2000US-0198123P.

PR 19-MAY-2000; 2000US-0205515P.

PR 07-JUN-2000; 2000US-0209467P.

PR 28-JUN-2000; 2000US-0214886P.

PR 30-JUN-2000; 2000US-0215135P.

PR 07-JUL-2000; 2000US-0216647P.

PR 07-JUL-2000; 2000US-0216880P.

PR 11-JUL-2000; 2000US-0217487P.

PR 11-JUL-2000; 2000US-0217496P.

PR 14-JUL-2000; 2000US-0218290P.

PR 26-JUL-2000; 2000US-0220963P.

PR 26-JUL-2000; 2000US-0220964P.

PR 14-AUG-2000; 2000US-0224518P.

PR 14-AUG-2000; 2000US-0225213P.

PR 14-AUG-2000; 2000US-0225214P.

PR 14-AUG-2000; 2000US-0225266P.

PR 14-AUG-2000; 2000US-0225267P.

PR 14-AUG-2000; 2000US-0225268P.

PR 14-AUG-2000; 2000US-0225270P.

PR 14-AUG-2000; 2000US-0225447P.

PR 14-AUG-2000; 2000US-0225757P.

PR 14-AUG-2000; 2000US-0225758P.

PR 14-AUG-2000; 2000US-0225759P.

PR 18-AUG-2000; 2000US-0226279P.

PR 22-AUG-2000; 2000US-0226681P.

PR 22-AUG-2000; 2000US-0226688P.

PR 22-AUG-2000; 2000US-0227182P.

PR 23-AUG-2000; 2000US-0227009P.

PR 30-AUG-2000; 2000US-0228924P.

PR 01-SEP-2000; 2000US-0229287P.

PR 01-SEP-2000; 2000US-0229343P.

PR 01-SEP-2000; 2000US-0229344P.

PR 01-SEP-2000; 2000US-0229345P.

PR 05-SEP-2000; 2000US-0229509P.

PR 05-SEP-2000; 2000US-0229513P.

PR 06-SEP-2000; 2000US-0230437P.

PR 06-SEP-2000; 2000US-0230438P.

PR 08-SEP-2000; 2000US-0231242P.

PR 08-SEP-2000; 2000US-0231243P.

PR 08-SEP-2000; 2000US-0231244P.

PR 08-SEP-2000; 2000US-0231413P.

PR 08-SEP-2000; 2000US-0231414P.

PR 08-SEP-2000; 2000US-0232080P.

PR 12-SEP-2000; 2000US-0232081P.

PR 14-SEP-2000; 2000US-0232397P.

PR 14-SEP-2000; 2000US-0232398P.

PR 14-SEP-2000; 2000US-0232399P.

PR 14-SEP-2000; 2000US-0232400P.

PR 14-SEP-2000; 2000US-0232401P.

PR 14-SEP-2000; 2000US-0233063P.

PR 14-SEP-2000; 2000US-0233064P.

PR 14-SEP-2000; 2000US-0233065P.

PR 21-SEP-2000; 2000US-0234223P.

PR 21-SEP-2000; 2000US-0234274P.

PR 25-SEP-2000; 2000US-0234997P.

PR 26-SEP-2000; 2000US-0234998P.

PR 26-SEP-2000; 2000US-0235484P.

PR 27-SEP-2000; 2000US-0235834P.

PR 27-SEP-2000; 2000US-0235836P.

PR 29-SEP-2000; 2000US-0236367P.

PR 29-SEP-2000; 2000US-0236368P.

PR 29-SEP-2000; 2000US-0236369P.

PR 29-SEP-2000; 2000US-0236370P.

PR 02-OCT-2000; 2000US-0236802P.

PR 02-OCT-2000; 2000US-0237037P.

PR 02-OCT-2000; 2000US-0237038P.

PR 02-OCT-2000; 2000US-0237039P.

PR 02-OCT-2000; 2000US-0237040P.

PR 13-OCT-2000; 2000US-0239935P.

PR 13-OCT-2000; 2000US-0239937P.

PR 20-OCT-2000; 2000US-0240960P.

PR 20-OCT-2000; 2000US-0241221P.

PR 20-OCT-2000; 2000US-0241785P.

PR 20-OCT-2000; 2000US-0241786P.

PR 20-OCT-2000; 2000US-0241787P.

PR 20-OCT-2000; 2000US-0241808P.

PR 20-OCT-2000; 2000US-0241809P.

PR 20-OCT-2000; 2000US-0241826P.

PR 01-NOV-2000; 2000US-0244617P.

PR 08-NOV-2000; 2000US-0246474P.

PR 08-NOV-2000; 2000US-0246475P.

PR 08-NOV-2000; 2000US-0246476P.

PR 08-NOV-2000; 2000US-0246477P.

PR 08-NOV-2000; 2000US-0246478P.

PR 08-NOV-2000; 2000US-0246523P.

PR 08-NOV-2000; 2000US-0246524P.

PR 08-NOV-2000; 2000US-0246525P.

PR 08-NOV-2000; 2000US-0246526P.

PR 08-NOV-2000; 2000US-0246527P.

PR 08-NOV-2000; 2000US-0246528P.

PR 08-NOV-2000; 2000US-0246532P.

PR 08-NOV-2000; 2000US-0246609P.

PR 08-NOV-2000; 2000US-0246610P.

PR 08-NOV-2000; 2000US-0246611P.

PR 08-NOV-2000; 2000US-0246613P.

PR 17-NOV-2000; 2000US-0249207P.

PR 17-NOV-2000; 2000US-0249208P.

PR 17-NOV-2000; 2000US-0249209P.

PR 17-NOV-2000; 2000US-0249210P.

PR 17-NOV-2000; 2000US-0249211P.

PR 17-NOV-2000; 2000US-0249212P.

PR 17-NOV-2000; 2000US-0249213P.

PR 17-NOV-2000; 2000US-0249214P.

PR 17-NOV-2000; 2000US-0249215P.

PR 17-NOV-2000; 2000US-0249216P.

PR 17-NOV-2000; 2000US-0249217P.

PR 17-NOV-2000; 2000US-0249218P.

PR 17-NOV-2000; 2000US-0249244P.

PR 17-NOV-2000; 2000US-0249245P.

PR 17-NOV-2000; 2000US-0249264P.

PR 17-NOV-2000; 2000US-0249265P.

PR 17-NOV-2000; 2000US-0249297P.

PR 17-NOV-2000; 2000US-0249299P.

PR 17-NOV-2000; 2000US-0249300P.

PR 01-DEC-2000; 2000US-0250160P.

PR 01-DEC-2000; 2000US-0250391P.

PR 05-DEC-2000; 2000US-0251030P.

PR 05-DEC-2000; 2000US-0251988P.

PR 05-DEC-2000; 2000US-0256719P.

PR 06-DEC-2000; 2000US-0251479P.

PR 08-DEC-2000; 2000US-0251856P.

PR 08-DEC-2000; 2000US-0251868P.

PR 08-DEC-2000; 2000US-0251869P.

PR 08-DEC-2000; 2000US-0251989P.  
PR 08-DEC-2000; 2000US-0251990P.  
PR 11-DEC-2000; 2000US-0254097P.  
PR 05-JAN-2001; 2001US-0259678P.  
PR 17-JAN-2001; 2001US-00764869.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Rosen CA, Ruben SM, Barash SC;  
PI  
XX  
XX WPI; 2003-743766/70.  
DR N-PSDB; ADE45576.  
DR  
XX  
XX  
PT New cardiovascular system related polynucleotides and polypeptides.  
PT useful for preventing, treating, or ameliorating a medical condition,  
PT such as cancer of cardiovascular tissues and cancer metastases.  
XX  
XX  
PS Claim 11; SEQ ID NO 997; 262pp; English.  
XX  
XX The invention relates to human cardiovascular system related polypeptides  
CC and the polynucleotides encoding them. The polypeptides, polynucleotides  
CC and antibodies to the polypeptides are useful for diagnosing a  
CC pathological condition or a susceptibility to a pathological condition,  
CC for preventing, treating, or ameliorating a medical condition, such as  
CC cancer of cardiovascular system tissues, proliferative disorders, foetal  
CC and developmental abnormalities, haematopoietic disorders, diseases of  
CC the immune system, AIDS, autoimmune diseases (e.g., rheumatoid  
CC arthritis), inflammation, allergies, neurological disorders (e.g.,  
CC Alzheimer's disease, Parkinson's disease), cognitive disorders,  
CC schizophrenia, asthma, skin disorders (e.g., psoriasis), sepsis,  
CC diabetes, atherosclerosis, cardiovascular disorders, angiogenic  
CC disorders, kidney disorders, gastrointestinal disorders, pregnancy-  
CC related disorders, endocrine disorders and infections. The nucleic acids  
CC are also useful for chromosome identification, radiation hybrid mapping  
CC or long-range restriction mapping. The polypeptides and polynucleotides  
CC may also be used as food additives or preservatives to increase or  
CC decrease storage capabilities, fat content or other nutritional  
CC components. This sequence represents a human cardiovascular system  
CC related polypeptide of the invention.  
XX  
XX Sequence 45 AA;  
Query Match 16.6%; Score 44.5; DB 7; Length 45;  
Best Local Similarity 38.5%; Pred. No. 2.7e-02;  
Matches 15; Conservative 1; Mismatches 12; Indels 11; Gaps 2;  
QY 9 QPALKYEGDPAPYKPKPERWYRASFPITVTAHSQTYRC 47  
DB 1 QPLLDKLGP-----WVTASIPLI--TGVHSGKNRC 28  
RESULT 16  
ADJ07609  
ID ADJ07609 standard; protein; 45 AA.  
XX  
XX ADJ07609;  
XX  
XX  
XX 04-NOV-2004 (first entry)  
XX  
XX Human cardiovascular system associated polypeptide SeqID997.  
XX autoimmune disease; rheumatoid arthritis; hyperproliferative disorder;  
XX breast neoplasms; liver neoplasms; cardiovascular disorder;  
XX cardiac arrest; cerebrovascular disorder; cerebral ischaemia;  
XX angiogenesis; nervous system disorder; Alzheimer's disease; infection;  
XX ocular disorder; corneal infection; wound healing;  
XX epithelial cell proliferation; skin aging; sunburn;  
XX organ transplantation; cell culture; tissue regeneration; chemotaxis;  
XX food additive; preservative; cardiovascular system associated antigen;  
XX nuclear factor kappaB; NFkappaB; promoter element; human.  
OS Homo sapiens.  
XX

PN  
XX  
PD  
XX  
XX  
PF 26-AUG-2002; 2002US-00227577.  
XX  
XX 31-JAN-2000; 2000US-0179065P.  
PR 04-FEB-2000; 2000US-0180628P.  
PR 24-FEB-2000; 2000US-0184664P.  
PR 02-MAR-2000; 2000US-0186350P.  
PR 16-MAR-2000; 2000US-0189874P.  
PR 17-MAR-2000; 2000US-0190076P.  
PR 18-APR-2000; 2000US-0198123P.  
PR 09-MAY-2000; 2000US-0205515P.  
PR 17-JUN-2000; 2000US-0209467P.  
PR 28-JUN-2000; 2000US-0214886P.  
PR 30-JUN-2000; 2000US-0215135P.  
PR 07-JUL-2000; 2000US-0216647P.  
PR 07-JUL-2000; 2000US-0216880P.  
PR 11-JUL-2000; 2000US-0217487P.  
PR 11-JUL-2000; 2000US-0217496P.  
PR 14-JUL-2000; 2000US-0218290P.  
PR 26-JUL-2000; 2000US-0220963P.  
PR 26-JUL-2000; 2000US-0220964P.  
PR 14-AUG-2000; 2000US-0224518P.  
PR 14-AUG-2000; 2000US-0224519P.  
PR 14-AUG-2000; 2000US-0225213P.  
PR 14-AUG-2000; 2000US-0225214P.  
PR 14-AUG-2000; 2000US-0225266P.  
PR 14-AUG-2000; 2000US-0225267P.  
PR 14-AUG-2000; 2000US-0225268P.  
PR 14-AUG-2000; 2000US-0225270P.  
PR 14-AUG-2000; 2000US-0225447P.  
PR 14-AUG-2000; 2000US-0225757P.  
PR 14-AUG-2000; 2000US-0225758P.  
PR 14-AUG-2000; 2000US-0225759P.  
PR 18-AUG-2000; 2000US-0226279P.  
PR 22-AUG-2000; 2000US-0226681P.  
PR 22-AUG-2000; 2000US-0226686P.  
PR 22-AUG-2000; 2000US-0227182P.  
PR 23-AUG-2000; 2000US-0227009P.  
PR 30-AUG-2000; 2000US-0228924P.  
PR 01-SEP-2000; 2000US-0229287P.  
PR 01-SEP-2000; 2000US-0229343P.  
PR 01-SEP-2000; 2000US-0229344P.  
PR 01-SEP-2000; 2000US-0229345P.  
PR 05-SEP-2000; 2000US-0229509P.  
PR 05-SEP-2000; 2000US-0229513P.  
PR 06-SEP-2000; 2000US-0230437P.  
PR 06-SEP-2000; 2000US-0230438P.  
PR 08-SEP-2000; 2000US-0231242P.  
PR 08-SEP-2000; 2000US-0231243P.  
PR 08-SEP-2000; 2000US-0231244P.  
PR 08-SEP-2000; 2000US-0231413P.  
PR 08-SEP-2000; 2000US-0231414P.  
PR 08-SEP-2000; 2000US-0232080P.  
PR 08-SEP-2000; 2000US-0232081P.  
PR 12-SEP-2000; 2000US-0231968P.  
PR 14-SEP-2000; 2000US-0232397P.  
PR 14-SEP-2000; 2000US-0232398P.  
PR 14-SEP-2000; 2000US-0232399P.  
PR 14-SEP-2000; 2000US-0232400P.  
PR 14-SEP-2000; 2000US-0232401P.  
PR 14-SEP-2000; 2000US-0233063P.  
PR 14-SEP-2000; 2000US-0233064P.  
PR 14-SEP-2000; 2000US-0233065P.  
PR 21-SEP-2000; 2000US-0234223P.  
PR 21-SEP-2000; 2000US-0234274P.  
PR 25-SEP-2000; 2000US-0234997P.  
PR 25-SEP-2000; 2000US-0234998P.  
PR 26-SEP-2000; 2000US-0235484P.  
PR 27-SEP-2000; 2000US-0235834P.  
PR 27-SEP-2000; 2000US-0235836P.

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PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 02-OCT-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 01-NOV-2000; 2000US-0241836P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 11-DEC-2000; 2000US-0251990P.
PR 05-JAN-2001; 2000US-0254097P.
PR 17-JAN-2001; 2001US-0259678P.
PR 07-MAR-2002; 2002US-00764869.
PR 07-MAR-2002; 2002US-00091504.
XX (HUMA-) HUMAN GENOME SCI INC.

XX PI Rosen CA, Ruben SM, Barash SC;
XX WPI; 2004-081713/08.
XX N-PSDB; ADJ06994.
XX New cardiovascular system-related nucleic acid molecule, useful for
PT diagnosing, preventing or treating diseases of the cardiovascular system,
PT and in chromosome mapping, drug screening or in pharmacogenomics.
XX Claim 11; SEQ ID NO 997; 262pp; English.
XX The invention relates to an isolated nucleic acid molecule encoding a
CC human cardiovascular system associated polypeptide (or antigens), or its
CC fragment. Also included recombinant vectors, recombinant host cells, an
CC isolated human cardiovascular system associated polypeptide (including
CC its fragment, allelic variant, species homologue or epitope), an isolated
CC antibody that binds specifically to a human cardiovascular system
CC associated polypeptide, diagnosing a pathological condition or
CC susceptibility to a pathological condition (comprising determining the
CC presence or absence of a mutation in human cardiovascular system
CC associated nucleic acid and diagnosing a condition based on the presence
CC or absence of the mutation), identifying a binding partner to human
CC cardiovascular system associated polypeptides, the gene corresponding to
CC the human cardiovascular system associated cDNA sequence and identifying
CC an activity in a biological assay comprising expressing the human
CC cardiovascular system associated cDNA in a cell, isolating the
CC supernatant, detecting an activity in a biological assay and identifying
CC the protein in the supernatant having the activity. The human
CC cardiovascular system associated nucleic acids and polypeptides are used
CC to prevent, treat or ameliorate a medical condition (for example in
CC humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep), for
CC example autoimmune diseases such as rheumatoid arthritis,
CC hyperproliferative disorders, for example neoplasms of the breast or

Query Match 16.6%; Score 44.5; DB 8; Length 45;
Best Local Similarity 38.5%; Pred. No. 2.7e+02;
Matches 15; Conservative 1; Mismatches 12; Indels 11; Gaps 2;

Qy 9 QPALKYEGDPAPYKNPERWYRASFPITVTAAHSGTYRC 47
Db 1 QFLLDKLG-----MVTASIPLI--TGVHSGKNRC 28

RESULT 17
AAW22399
ID AAW22399 standard; peptide; 26 AA.
XX AC AAW22399;
XX DT 08-OCT-1997 (first entry)
XX DE Soluble CD14 protein amino acids 143-168.
XX KW Soluble; CD14; glycerophosphoinositol anchored membrane protein; infection;
XX cell surface; neutrophil; lipopolysaccharide; bacterium; interleukin;
XX tumour necrosis factor-alpha; growth; invasiveness; pathogenic; monocytic;
XX dissemination; bloodstream; peritoneal cavity; bacteraemia; antagonist;
XX gastrointestinal tract; septicaemia; appendicitis; gastroenteritis;
XX inflammatory bowel disease; peritonitis.
XX OS Homo sapiens.
XX FN W09700081-A1.
XX PD 03-JAN-1997.
XX PF 19-JUN-1996; 96WO-US010803.
XX PR 19-JUN-1995; 95US-00491759.
XX PA (GOYE/) GOYERT S M.
XX
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PI Goyert SM;  
 XX WPI; 1997-077357/07.  
 XX  
 XX Use of a CD14 antagonist - for preventing or treating bacteraemia or for  
 PT preventing the translocation of bacteria.  
 XX  
 XX Disclosure; Page 8; 62pp; English.  
 XX  
 CC This peptide represents amino acids 143-168 of the soluble form of the 55  
 CC kD CD14 glycoprophosphoinositol (GPI) anchored membrane protein. The protein  
 CC is expressed strongly on the surface of monocytes and weakly on the  
 CC surface of neutrophils. CD14 binds lipopolysaccharides (LPS), especially  
 CC of bacterial origin, and binding causes cells to become highly activated  
 CC and release interleukins such as tumour necrosis factor-alpha. One side  
 CC effect of interleukin release is that it promotes growth and invasiveness  
 CC of pathogenic bacteria, allowing their dissemination into the bloodstream  
 CC and peritoneal cavity. The invention relates to methods for preventing or  
 CC treating bacteraemia in a patient or preventing the translocation of  
 CC bacteria from the gastrointestinal tract, by administering a CD14  
 CC antagonist, preferably a dipeptide which binds LPS, LPS binding protein  
 CC or LPS-LPS binding protein complex. The methods are especially useful for  
 CC controlling severe local infections, preventing and treating bacteraemia  
 CC and septicemia e.g. for peritonitis, appendicitis, gastroenteritis,  
 CC inflammatory bowel diseases, etc  
 XX  
 XX Sequence 26 AA;  
 SQ

Query Match 16.4%; Score 44; DB 2; Length 26;  
 Best Local Similarity 21.7%; Pred. No. 1.6e+02;  
 Matches 5; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 25 ERWRASFPPIITVTAHSGTYRC 47  
 : : : : :  
 Db 4 QQWLKPKGLKVLSTIAQAHSINFS 26

RESULT 18  
 AA75901  
 ID AA75901 standard; peptide; 26 AA.  
 XX  
 AC AA75901;  
 XX  
 DT 10-NOV-1998 (first entry)  
 XX  
 DE Recombinant human CD14 (rsCD14) peptide fragment (residues 143-168).  
 XX  
 KW CD14; recombinant; human; rsCD14; lipopolysaccharide; LPS;  
 KW LPS binding activity; treatment; sepsis; Gram-negative bacteraemia;  
 KW autoimmune disease; tissue rejection; Gram-negative bacterial sepsis.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN US5804189-A.  
 XX  
 PD 08-SEP-1998.  
 XX  
 PF 06-JUN-1994; 94US-00254095.  
 XX  
 PR 06-APR-1992; 92US-00863913.  
 XX  
 PA (GOYE/) GOYERT S M.  
 XX  
 PI Goyert SM;  
 XX  
 XX WPI; 1998-505586/43.  
 DR  
 XX Treatment of lipo-polysaccharide-mediated conditions - by administering  
 PT soluble CD14 fragment.  
 XX  
 PS Claim 12; Col 20; 18pp; English.  
 XX

CC This sequence represents a soluble recombinant human CD14 (rsCD14)  
 CC peptide fragment that has a lipopolysaccharide (LPS) binding activity.  
 CC The invention provides a method for the prevention and treatment of a  
 CC condition mediated by the action of LPS or membrane-bound CD14 that  
 CC comprises administering this soluble mammalian CD14 fragment having LPS  
 CC binding activity. The method is used for preventing or treating sepsis,  
 CC Gram-negative bacteraemia, autoimmune diseases or tissue rejection,  
 CC especially Gram-negative bacterial sepsis  
 XX  
 SQ Sequence 26 AA;  
 Query Match 16.4%; Score 44; DB 2; Length 26;  
 Best Local Similarity 21.7%; Pred. No. 1.6e+02;  
 Matches 5; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 25 ERWRASFPPIITVTAHSGTYRC 47  
 : : : : :  
 Db 4 QQWLKPKGLKVLSTIAQAHSINFS 26

RESULT 19  
 ADS88820  
 ID ADS88820 standard; peptide; 26 AA.  
 XX  
 AC ADS88820;  
 XX  
 DT 16-DEC-2004 (first entry)  
 XX  
 DE Amino acid sequence of a soluble CD14 (sCD14) peptide.  
 XX  
 KW myeloid cell-surface glycoprotein; CD14; soluble CD14; sCD14;  
 KW lipopolysaccharide blocker; insulin resistance; blood glucose level;  
 KW chronic inflammatory disease; type 2 diabetes mellitus; obesity;  
 KW metabolic syndrome; arteriosclerotic disease; arterial hypertension;  
 KW functional ovarian hyperandrogenism; dyslipidaemia;  
 KW coagulation alternation; hyperuricaemia.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004082578-A2.  
 XX  
 PD 30-SEP-2004.  
 XX  
 PF 23-FEB-2004; 2004WO-EP050189.  
 XX  
 PR 21-MAR-2003; 2003ES-00000565.  
 PR 16-DEC-2003; 2003EP-00104722.  
 XX  
 PA (MELL-) MELLITUS SL.  
 XX  
 PI Fernandez-Real J, Engel W;  
 XX  
 DR WPI; 2004-699692/68.  
 XX  
 XX Use of soluble myeloid cell-surface glycoprotein in the treatment or  
 PT prevention of chronic inflammatory conditions and clinical disorders of  
 PT insulin resistance e.g. type 2 diabetes and obesity.  
 XX  
 PS Claim 9; SEQ ID NO 1; 19pp; English.  
 XX  
 CC The present sequence represents a fragment of a soluble myeloid cell-  
 CC surface glycoprotein (soluble CD14, (sCD14)), comprising residues 143-168  
 CC of the human recombinant sCD14 sequence. sCD14 is potent  
 CC lipopolysaccharide blocker that improves insulin resistance in diabetic  
 CC patients and normalizes blood glucose levels. The present sCD14 peptide  
 CC is used for the manufacture of a medicament for treatment or prevention  
 CC of chronic inflammatory conditions and clinical disorders associated with  
 CC insulin resistance. These include type 2 diabetes mellitus, obesity,  
 CC metabolic syndrome, arteriosclerotic disease, arterial hypertension,  
 CC functional ovarian hyperandrogenism, dyslipidaemia, coagulation  
 CC alternations and hyperuricaemia.  
 XX  
 XX Sequence 26 AA;  
 SQ



XX AC ADI46793;  
XX DT 06-MAY-2004 (first entry)  
XX DE Permeabilising peptide of human JAM-1 SeqID502.  
XX KW mucosal delivery; permeabilising peptide;  
KW mucosal epithelial paracellular transport; epithelial junction;  
KW epithelial membrane adhesive protein; junctional adhesion molecule; JAM;  
KW occludin; claudin; sexual dysfunction; male erectile sexual dysfunction;  
KW female sexual dysfunction; human.  
XX OS Homo sapiens.  
XX FN WO2004003145-A2.  
XX PD 08-JAN-2004.  
XX PF 24-JUN-2003; 2003WO-US019994.  
XX PR 28-JUN-2002; 2002US-0392512P.  
XX PA (NAST-) NASTECH PHARM CO INC.  
XX PY Quay SC;  
XX WI WIPI; 2004-091087/09.  
XX CC Composition comprising biologically active agent and permeabilizing  
PT peptide that reversibly enhances mucosal epithelial paracellular  
PT transport by modulating epithelial junctional structure and/or physiology  
PT in mammal.  
XX PS Disclosure; SEQ ID NO 502; 426pp; English.  
XX CC This invention relates to a novel composition comprising a biologically  
CC active agent and mucosal delivery-enhancing effective amount of  
CC permeabilising peptide that reversibly enhances mucosal epithelial  
CC paracellular transport by modulating epithelial junctional structure  
CC and/or physiology in a mammal. The agent of the invention inhibits  
CC homotypic binding of epithelial membrane adhesive protein chosen  
CC junctional adhesion molecule (JAM), occludin and claudin. The  
CC biologically active agent is effective for treatment of sexual  
CC dysfunction, for example male erectile sexual dysfunction or female  
CC sexual dysfunction. The present sequence is that of a permeabilising  
CC peptide of human JAM-1 which may be used during the production of the  
CC composition of the invention.  
XX SQ Sequence 13 AA;  
Query Match 16.0%; Score 43; DB 8; Length 13;  
Best Local Similarity 66.7%; Pred. No. 91;  
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 36 TWTAAHSGTYRC 47  
DB 1 SVTREDSGTYRC 12  
RESULT 23  
ADI46809  
ID ADI46809 standard; peptide; 13 AA.  
AC ADI46809;  
XX 06-MAY-2004 (first entry)  
XX DE Permeabilising peptide of human JAM-1 SeqID518.  
XX KW mucosal delivery; permeabilising peptide;  
KW mucosal epithelial paracellular transport; epithelial junction;  
KW epithelial membrane adhesive protein; junctional adhesion molecule; JAM;  
KW epithelial junctional structure and/or physiology

KW occludin; claudin; sexual dysfunction; male erectile sexual dysfunction;  
KW female sexual dysfunction; human.  
XX OS Homo sapiens.  
XX FN WO2004003145-A2.  
XX PD 08-JAN-2004.  
XX PF 24-JUN-2003; 2003WO-US019994.  
XX PR 28-JUN-2002; 2002US-0392512P.  
XX PA (NAST-) NASTECH PHARM CO INC.  
XX PY Quay SC;  
XX WI WIPI; 2004-091087/09.  
XX CC Composition comprising biologically active agent and permeabilizing  
PT peptide that reversibly enhances mucosal epithelial paracellular  
PT transport by modulating epithelial junctional structure and/or physiology  
PT in mammal.  
XX PS Disclosure; SEQ ID NO 518; 426pp; English.  
XX CC This invention relates to a novel composition comprising a biologically  
CC active agent and mucosal delivery-enhancing effective amount of  
CC permeabilising peptide that reversibly enhances mucosal epithelial  
CC paracellular transport by modulating epithelial junctional structure  
CC and/or physiology in a mammal. The agent of the invention inhibits  
CC homotypic binding of epithelial membrane adhesive protein chosen  
CC junctional adhesion molecule (JAM), occludin and claudin. The  
CC biologically active agent is effective for treatment of sexual  
CC dysfunction, for example male erectile sexual dysfunction or female  
CC sexual dysfunction. The present sequence is that of a permeabilising  
CC peptide of human JAM-1 which may be used during the production of the  
CC composition of the invention.  
XX SQ Sequence 13 AA;  
Query Match 16.0%; Score 43; DB 8; Length 13;  
Best Local Similarity 66.7%; Pred. No. 91;  
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 36 TWTAAHSGTYRC 47  
DB 1 SVTREDSGTYRC 12  
RESULT 24  
ADP86970  
ID ADP86970 standard; peptide; 13 AA.  
AC ADP86970;  
XX 09-SEP-2004 (first entry)  
XX DE Junctional adhesion molecule 1 (JAM-1) peptide seqid 375.  
XX KW anorectic; cytostatic; eating disorder; neuroprotective; nootropic;  
KW cachexia; intranasal composition; peptide YV; obesity; cancer;  
KW malnutrition; wasting; Alzheimer's disease; colon adenocarcinoma;  
KW pancreatic adenocarcinoma; breast carcinoma; cachexia; cancer cachexia;  
KW junctional adhesion molecule 1; JAM-1; epithelial junction; human.  
XX OS Homo sapiens.  
XX FN US2004115135-A1.  
XX PD 17-JUN-2004.  
XX PR 17-DEC-2002; 2002US-00322266.

XX 17-DEC-2002; 2002US-00322266.  
 XX (QUAY/) QUAY S C.  
 XX Quay SC;  
 XX WPI; 2004-478989/45.  
 XX Intranasal compositions for treating obesity, cancer, or malnutrition or  
 PT wasting related to cancer, comprises peptide compound(s) formulated for  
 PT mucosal delivery to mammalian subject.  
 XX Disclosure; SEQ ID NO 375; 86pp; English.  
 XX The invention describes an intranasal composition comprising peptide YY  
 CC compound(s) formulated for mucosal delivery to a mammalian subject. Also  
 CC described is a kit for treatment of a mammalian subject comprising the  
 CC intranasal composition of peptide compound(s). The composition is used  
 CC for treating obesity, cancer, or malnutrition or wasting related to  
 CC cancer in the subject. It is used to alleviate Alzheimer's disease, colon  
 CC adenocarcinoma, pancreatic adenocarcinoma, breast carcinoma, treatment  
 CC and prevention of malnutrition resulting from iatrogenic causes or  
 CC cachexia associated with advanced disease, or cancer cachexia in the  
 CC subject. The composition alleviates the symptoms without unacceptable  
 CC adverse side effects. This is the amino acid sequence of a human  
 CC junctional adhesion molecule 1 (JAM-1) that may be used in a composition  
 CC of the invention to modulate epithelial junction structure and/or  
 CC physiology.  
 XX Sequence 13 AA;  
 SQ

Query Match 16.0%; Score 43; DB 8; Length 13;  
 Best Local Similarity 66.7%; Pred. No. 91;  
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 Qy 36 TVTAHSGTYRC 47  
 :||| |||||  
 Db 1 SVTREDSGTYRC 12

RESULT 25  
 ADP86986  
 ID ADP86986 standard; peptide; 13 AA.  
 XX  
 AC ADP86986;  
 XX  
 DT 09-SEP-2004 (first entry)  
 XX  
 DE Junctional adhesion molecule 1 (JAM-1) peptide seqid 391.  
 XX  
 KW anorectic; cytostatic; eating disorder; neuroprotective; nootropic;  
 KW cachexia; intranasal composition; peptide YY; obesity; cancer;  
 KW malnutrition; wasting; Alzheimer's disease; colon adenocarcinoma;  
 KW pancreatic adenocarcinoma; breast carcinoma; cachexia; cancer cachexia;  
 KW junctional adhesion molecule 1; JAM-1; epithelial junction; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2004115135-A1.  
 XX  
 PD 17-JUN-2004.  
 XX  
 PF 17-DEC-2002; 2002US-00322266.  
 XX  
 PR 17-DEC-2002; 2002US-00322266.  
 XX  
 PA (QUAY/) QUAY S C.  
 XX  
 FI Quay SC;  
 XX  
 DR WPI; 2004-478989/45.  
 XX

PT Intranasal compositions for treating obesity, cancer, or malnutrition or  
 PT wasting related to cancer, comprises peptide compound(s) formulated for  
 PT mucosal delivery to mammalian subject.  
 XX Disclosure; SEQ ID NO 391; 86pp; English.  
 XX The invention describes an intranasal composition comprising peptide YY  
 CC compound(s) formulated for mucosal delivery to a mammalian subject. Also  
 CC described is a kit for treatment of a mammalian subject comprising the  
 CC intranasal composition of peptide compound(s). The composition is used  
 CC for treating obesity, cancer, or malnutrition or wasting related to  
 CC cancer in the subject. It is used to alleviate Alzheimer's disease, colon  
 CC adenocarcinoma, pancreatic adenocarcinoma, breast carcinoma, treatment  
 CC and prevention of malnutrition resulting from iatrogenic causes or  
 CC cachexia associated with advanced disease, or cancer cachexia in the  
 CC subject. The composition alleviates the symptoms without unacceptable  
 CC adverse side effects. This is the amino acid sequence of a human  
 CC junctional adhesion molecule 1 (JAM-1) that may be used in a composition  
 CC of the invention to modulate epithelial junction structure and/or  
 CC physiology.  
 XX Sequence 13 AA;  
 SQ

Query Match 16.0%; Score 43; DB 8; Length 13;  
 Best Local Similarity 66.7%; Pred. No. 91;  
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 Qy 36 TVTAHSGTYRC 47  
 :||| |||||  
 Db 1 SVTREDSGTYRC 12

Search completed: October 29, 2005, 04:24:10  
 Job time : 170 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 29, 2005, 04:18:41 ; Search time 42 Seconds  
(without alignments)  
83.536 Million cell updates/sec

Title: US-09-503-387-3\_COPY\_134\_180

Perfect score: 268

Sequence: 1 CQRYGDFQALYKEGPAP.....YRASFPITVTAHSGTYRC 47

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 270212

Minimum DB seq length: 0

Maximum DB seq length: 48

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents AA.\*

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2: /cgn2\_6/ptodata/1/iaa/5B.COMB.pap.\*

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4: /cgn2\_6/ptodata/1/iaa/6B.COMB.pap.\*

5: /cgn2\_6/ptodata/1/iaa/PCTUS.COMB.pap.\*

6: /cgn2\_6/ptodata/1/iaa/backfiles1.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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11	43	16.0	41	3	US-09-345-468-22
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14	42	15.7	30	4	US-09-205-258-646
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16	41	15.3	39	4	US-09-079-723-41
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18	40.5	15.1	43	2	US-08-332-562A-21
19	40	14.9	36	4	US-10-027-038-5
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21	39	14.6	36	3	US-09-248-082-10
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					Sequence 18, Appli

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39	35	13.1	24	2	US-08-484-631-114	Sequence 114, App
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53	35	13.1	46	3	US-09-211-590-4	Sequence 4, Appli
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## ALIGNMENTS

RESULT 1  
US-09-345-468-7

; Sequence 7, Application US/09345468  
; Patent No. 6245527

; GENERAL INFORMATION:

; APPLICANT: Busfield, S.

; APPLICANT: Villevall, J.

; APPLICANT: Jandrot-Perrus, M.

; APPLICANT: Vaichenker, W.

; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF

; FILE REFERENCE: 7853-147

; CURRENT APPLICATION NUMBER: US/09/345,468

; CURRENT FILING DATE: 1999-06-30

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 7

; LENGTH: 47

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-345-468-7

Query Match

Best Local Similarity 100.0%; Score 268; DB 3; Length 47;

; Patent No. 3.8e-31;

Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CQTRYGDFQALYKEGDPAPYKNPERWYRASFPFIITVTAHSGTYRC 47

RESULT 2

US-09-414-453A-7

; Sequence 7, Application US/09414453A

; Patent No. 6383779

; GENERAL INFORMATION:

; APPLICANT: Busfield, S.

; APPLICANT: Villevall, J.

; APPLICANT: Jandrot-Perrus, M.

; APPLICANT: Vaichenker, W.

; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF

; FILE REFERENCE: 7853-147

; CURRENT APPLICATION NUMBER: US/09/414,453A

; CURRENT FILING DATE: 1999-10-07

; PRIOR APPLICATION NUMBER: 09/345,468

; PRIOR FILING DATE: 1999-06-30

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 7

; LENGTH: 47

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-414-453A-7

Query Match

Best Local Similarity 100.0%; Score 268; DB 3; Length 47;

; Patent No. 3.8e-31;

Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CQTRYGDFQALYKEGDPAPYKNPERWYRASFPFIITVTAHSGTYRC 47

Db 1 CQTRYGDFQALYKEGDPAPYKNPERWYRASFPFIITVTAHSGTYRC 47

RESULT 3

US-09-345-468-23

; Sequence 23, Application US/09345468

; Patent No. 6245527

; GENERAL INFORMATION:

; APPLICANT: Busfield, S.

; APPLICANT: Villevall, J.

; APPLICANT: Jandrot-Perrus, M.

; APPLICANT: Vaichenker, W.

; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF

; FILE REFERENCE: 7853-147

; CURRENT APPLICATION NUMBER: US/09/345,468

; CURRENT FILING DATE: 1999-06-30

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 23

; LENGTH: 47

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-345-468-23

Query Match

Best Local Similarity 82.1%; Score 220; DB 3; Length 47;

; Patent No. 2.8e-24;

Matches 37; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

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Db 1 CQSPYSDFEVLKEDTGPYKPKWYRANFFIITVTAHSGTYRC 47

RESULT 4

US-09-414-453A-23

; Sequence 23, Application US/09414453A

; Patent No. 6383779

; GENERAL INFORMATION:

; APPLICANT: Busfield, S.

; APPLICANT: Villevall, J.

; APPLICANT: Jandrot-Perrus, M.

; APPLICANT: Vaichenker, W.

; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF

; FILE REFERENCE: 7853-147

; CURRENT APPLICATION NUMBER: US/09/414,453A

; CURRENT FILING DATE: 1999-10-07

; PRIOR APPLICATION NUMBER: 09/345,468

; PRIOR FILING DATE: 1999-06-30

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 23

; LENGTH: 47

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-414-453A-23

Query Match

Best Local Similarity 82.1%; Score 220; DB 3; Length 47;

; Patent No. 2.8e-24;

Matches 37; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

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Db 1 CQSPYSDFEVLKEDTGPYKPKWYRANFFIITVTAHSGTYRC 47

RESULT 5

US-08-726-306A-119

; Sequence 119, Application US/08726306A

; Patent No. 5958684

; GENERAL INFORMATION:

; APPLICANT: van Leeuwen, Frederik Willem

; APPLICANT: Burbach, Johannes Peter Henri

; APPLICANT: Grosveld, Franklin G.

; TITLE OF INVENTION: DIAGNOSIS METHOD AND REAGENTS

; NUMBER OF SEQUENCES: 189

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Banner & Witcoff, Ltd.

; STREET: 1 Financial Center

; CITY: Boston

; STATE: MA

; COUNTRY: US

; ZIP: 02111

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,306A
FILING DATE: 02-Oct-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 95/20080.4
FILING DATE: 02-Oct-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/009,832
FILING DATE: 01-Jan-1996
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Ph.D., Kathleen M.
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 96,048-A (3255/00784)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 345-9100
TELEFAX: (617) 345-9111
INFORMATION FOR SEQ ID NO: 119:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-726-306A-119

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Query Match	17.4%	Score	46.5	DB 2	Length	38			
Best Local Similarity	58.8%	Pred. No.	14						
Matches	10	Conservative	1	Mismatches	5	Indels	1	Gaps	1

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Db 3 HPEGVDPAFGPASERWY 19

RESULT 6  
US-08-726-306A-122  
; Sequence 122, Application US/08726306A  
; Patent No. 5958684  
; GENERAL INFORMATION:  
; APPLICANT: van Leeuwen, Frederik Willem  
; APPLICANT: Burbach, Johannes Peter Henri  
; APPLICANT: Grosveld, Franklin G.  
; TITLE OF INVENTION: DIAGNOSIS METHOD AND REAGENTS  
; NUMBER OF SEQUENCES: 189  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Banner & Witcoff, Ltd.  
; STREET: 1 Financial Center  
; CITY: Boston  
; STATE: MA  
; COUNTRY: US  
; ZIP: 02111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WordPerfect 6.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/726,306A  
; FILING DATE: 02-Oct-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 95/20080.4  
; FILING DATE: 02-Oct-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/009,832  
; FILING DATE: 01-Jan-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Williams, Ph.D., Kathleen M.  
; REGISTRATION NUMBER: 34,380

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1 / REFERENCE/DOCKET NUMBER: 36,048-A (3255/00784)
2 / TELECOMMUNICATION INFORMATION:
3 / TELEPHONE: (617) 345-9100
4 / TELEFAX: (617) 345-9111
5 / INFORMATION FOR SEQ ID NO: 122:
6 / SEQUENCE CHARACTERISTICS:
7 / LENGTH: 38 amino acids
8 / TYPE: amino acid
9 / STRANDEDNESS: single
10 / TOPOLOGY: unknown
11 / MOLECULE TYPE: peptide
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Query Match      17.2%; Score 46; DB 2; Length 42;
Best Local Similarity 48.0%; Pred. No. 19;
Matches 12; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

Qy 18 PAPYKNPERWYRASFPITVTAHNS 42
   ||| | | | | | | | | | | | | |
Db 11 PAPSTSPSPWRASRPRTAPAPS 35

RESULT 8
US-08-254-095-1
; Sequence 1, Application US/08254095
; Patent No. 5804189
; GENERAL INFORMATION:
; APPLICANT: Goyert, Sanna S.
; TITLE OF INVENTION: A No. 5804189el Thgerapy for Treating Symptoms
; TITLE OF INVENTION: Of Sepsis Using A Soluble Form of Recombinant CD14
; TITLE OF INVENTION: Myelomonocytic Antigen
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: One Broadway
; CITY: New York
; STATE: N.Y.
; COUNTRY: U.S.A.
; ZIP: 10004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/254.095
; APPLICATION NUMBER: US/08/254.095
; FILING DATE: 06-JUN-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/863,913
; FILING DATE: 06-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Sinder, Stuart J
; REFERENCE/DOCKET NUMBER: 52492/1002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 425-7200
; TELEFAX: (212) 425-5288
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
;
US-08-254-095-1

Query Match      16.4%; Score 44; DB 1; Length 26;
Best Local Similarity 21.7%; Pred. No. 20;
Matches 5; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

Qy 25 ERWYRASFPITVTAHNSGTYRC 47
   :| | :| | :| | :| | :| |
Db 4 QQWLKPKGLKVLISIAQAHSNLFSC 26

RESULT 9
US-09-132-769-17
; Sequence 17, Application US/09132769A
; Patent No. 6525023
; GENERAL INFORMATION:
; APPLICANT: Motoo Yamasaki
; APPLICANT: Kenji Shibata
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; APPLICANT: No. 6525023uo Hanai
; APPLICANT: Akiko Furuya
; APPLICANT: Kaoru Miyamoto
; TITLE OF INVENTION: NOVEL VASCULAR SMOOTH MUSCLE CELL GROWTH FACTOR
; FILE REFERENCE: 11078
; CURRENT APPLICATION NUMBER: US/09/132,769A
; CURRENT FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: HEI9-218491
; EARLIER FILING DATE: 1997-08-13
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 17
; LENGTH: 30
; TYPE: PRT
; ORGANISM: BOVINE
;
US-09-132-769-17

Query Match      16.4%; Score 44; DB 4; Length 30;
Best Local Similarity 53.3%; Pred. No. 24;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 4 RYGFDPQFALYKEGDP 18
   | | : | | | | |
Db 16 REGYTEFSLRVEGDP 30

RESULT 10
US-09-043-731-13
; Sequence 13, Application US/09043731A
; Patent No. 6344203
; GENERAL INFORMATION:
; APPLICANT: The Austin Research Institute
; TITLE OF INVENTION: Mimicking Peptides in Cancer Therapy
; FILE REFERENCE: CALA-200
; CURRENT APPLICATION NUMBER: US/09/043,731A
; CURRENT FILING DATE: 1998-06-23
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 13
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: single
; OTHER INFORMATION: stranded linear peptide
;
US-09-043-731-13

Query Match      16.0%; Score 43; DB 3; Length 28;
Best Local Similarity 40.0%; Pred. No. 31;
Matches 8; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Qy 28 YRASFPITVTAHNSGTYRC 47
   | : | | | | | | | |
Db 5 YSGNFSIPKANSHSGDYIC 24

RESULT 11
US-09-345-468-22
; Sequence 22, Application US/09345468
; Patent No. 6245527
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Villeva, J.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-147
; CURRENT APPLICATION NUMBER: US/09/345,468
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Fast-SEQ for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 41
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; TYPE: PRT
; ORGANISM: Mus musculus
US-09-345-468-22

Query Match      16.0%; Score 43; DB 3; Length 41;
Best Local Similarity 29.2%; Pred. No. 50;
Matches 14; Conservative 7; Mismatches 19; Indels 8; Gaps 2;

Qy 1 CQRYGDFQFALYKGDPAKYKPERWYRASFPPII-TVTAHSGTYRC 47
Db 1 CQGPDPVDLYRLEK-----LKPEKYEDQDFLFIPTMERSNAGTYRC 41

RESULT 12
US-09-414-453A-22
; Sequence 22, Application US/09414453A
; Patent No. 6383779
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Villevall, J.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Vaanchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-147
; CURRENT APPLICATION NUMBER: US/09/414,453A
; CURRENT FILING DATE: 1999-10-07
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-414-453A-22

Query Match      16.0%; Score 43; DB 3; Length 41;
Best Local Similarity 29.2%; Pred. No. 50;
Matches 14; Conservative 7; Mismatches 19; Indels 8; Gaps 2;

Qy 1 CQRYGDFQFALYKGDPAKYKPERWYRASFPPII-TVTAHSGTYRC 47
Db 1 CQGPDPVDLYRLEK-----LKPEKYEDQDFLFIPTMERSNAGTYRC 41

RESULT 13
US-08-332-562A-22
; Sequence 22, Application US/08332562A
; Patent No. 5985599
; GENERAL INFORMATION:
; APPLICANT: MCKENZIE, Ian F.C.
; APPLICANT: HOGARTH, Mark P.
; APPLICANT: HIBBS, Margaret L.
; APPLICANT: SCOTT, Bernadette M.
; APPLICANT: BONADONNA, Lisa
; APPLICANT: HULETT, Mark D.
; TITLE OF INVENTION: FC RECEPTOR FOR IMMUNOGLOBULIN
; NUMBER OF SEQUENCES: 136
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/332,562A
; FILING DATE: 31-OCT-1994

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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; FILING DATE: 27-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 54270/119/GRHA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-332-562A-22

Query Match      16.0%; Score 43; DB 2; Length 45;
Best Local Similarity 40.0%; Pred. No. 56;
Matches 8; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Qy 28 YRASFPPIITVTAHSGTYRC 47
Db 26 YSSNFSIPKANSHSGDYIC 45

RESULT 14
US-09-205-258-646
; Sequence 646, Application US/09205258
; Patent No. 5525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06

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EARLIER APPLICATION NUMBER: 60/048,901  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,892  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,915  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,019  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,970  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,972  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,916  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,373  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,875  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,374  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,917  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,949  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,974  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,883  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,897  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,898  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,962  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,963  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,877  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,878  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/070,923  
EARLIER FILING DATE: 1997-12-18  
EARLIER APPLICATION NUMBER: 60/092,921  
EARLIER FILING DATE: 1998-07-15  
EARLIER APPLICATION NUMBER: 60/094,657  
EARLIER FILING DATE: 1998-07-30  
NUMBER OF SEQ ID NOS: 1227  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 646  
LENGTH: 30  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-205-258-646

Query Match 15.7%; Score 42; DB 4; Length 30;  
Best Local Similarity 34.3%; Pred. No. 47;  
Matches 12; Conservative 4; Mismatches 9; Indels 10; Gaps 3;  
Qy 1 COT-RYGFDPALYKEGDPAPYKPNRWYASFPI 34  
Db 4 CLTVRWAFESLQV-----PQNPFRW--ASHPL 29  
RESULT 15  
US-09-443-780C-57  
Sequence 57, Application US/09443780C  
Patent No. 6699273  
GENERAL INFORMATION:  
APPLICANT: O'Mahony, Daniel J  
APPLICANT: Seveso, Michela  
TITLE OF INVENTION: Antibodies To Peptides That Target GIT Receptors And Related Meth  
FILE REFERENCE: E1067/20037  
CURRENT APPLICATION NUMBER: US/09/443,780C

CURRENT FILING DATE: 1999-11-19  
PRIOR APPLICATION NUMBER: US 60/109,036  
PRIOR FILING DATE: 1998-11-19  
NUMBER OF SEQ ID NOS: 84  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 57  
LENGTH: 39  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: PAX45 39 mer fragment L-form  
US-09-443-780C-57  
Query Match 15.3%; Score 41; DB 4; Length 39;  
Best Local Similarity 38.5%; Pred. No. 91;  
Matches 10; Conservative 4; Mismatches 10; Indels 2; Gaps 1;  
Qy 5 YGFDQPALYKEGDPAPYKPNRWYRA 30  
Db 8 HGLERHAL--DGTGPLYAMPGRWLRA 31  
RESULT 16  
US-09-079-723-41  
Sequence 41, Application US/09079723  
Patent No. 6703362  
GENERAL INFORMATION:  
APPLICANT: Alvarez, Vernon L.  
APPLICANT: O'Mahony, Daniel J.  
APPLICANT: Lambkin, Imelda J.  
APPLICANT: Singleton, Judith  
APPLICANT: Patterson, Catherine A.  
APPLICANT: Cagney, Gerard M.  
APPLICANT: Belinka, Benjamin A.  
APPLICANT: Carter, John M.  
TITLE OF INVENTION: RANDOM PEPTIDES THAT BIND TO GASTRO-  
INTESTINAL TRACT (GIT) TRANSPORT RECEPTORS AND RELATED METHODS  
NUMBER OF SEQUENCES: 265  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/079,723  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Misrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-219  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 39 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-09-079-723-41  
Query Match 15.3%; Score 41; DB 4; Length 39;  
Best Local Similarity 38.5%; Pred. No. 91;

QY 16 GDPAPYKNPERWYRASFPITVTAAH 41

Db 9 GDPAPVEDLIRFYDNLQQLNVVTRH 34

RESULT 20  
US-08-251-472-10  
; Sequence 10, Application US/08251472  
; Patent No. 5871746  
; GENERAL INFORMATION:  
; APPLICANT: BOUTILLON, CHRISTOPHE; MARTINON,  
; APPLICANT: FREDERIC; GRAS-MASSE, HELENE;  
; APPLICANT: GOMARD, ELISABETH; SERGHERAERT,  
; APPLICANT: CHRISTIAN; MAGNE, REMY; TARTAR,  
; APPLICANT: ANDRE; LEVY, JEAN-PAUL  
; TITLE OF INVENTION: CYTOTOXIC T LYMPHOCYTE  
; TITLE OF INVENTION: -INDUCING LIPOPEPTIDES AND USE AS VACCINES  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIERMAN & MUSERLIAN  
; STREET: 600 THIRD AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10016  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY DISK  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/251,472  
; FILING DATE: 31-MAY-1994  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MUSERLIAN, CHARLES A  
; REGISTRATION NUMBER: 19,683  
; REFERENCE/DOCKET NUMBER: 102.1511  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 661-8000  
; TELEFAX: (212) 661-8002  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 36  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
; ORIGINAL SOURCE:  
; ORGANISM: SIV  
; FEATURE:  
; LOCATION: GAG 246-281  
; US-08-251-472-10

Query Match 14.6%; Score 39; DB 2; Length 36;  
Best Local Similarity 37.5%; Pred. No. 1.6e+02;  
Matches 6; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 12 LYKEGDPAPYKNPERW 27  
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Db 5 MYRQNPVPVGNIRW 20

RESULT 21  
US-09-248-082-10  
; Sequence 10, Application US/09248082  
; Patent No. 6015564  
; GENERAL INFORMATION:  
; APPLICANT: BOUTILLON, CHRISTOPHE; MARTINON,  
; APPLICANT: FREDERIC; GRAS-MASSE, HELENE;  
; APPLICANT: GOMARD, ELISABETH; SERGHERAERT,  
; APPLICANT: CHRISTIAN; MAGNE, REMY; TARTAR,  
; APPLICANT: ANDRE; LEVY, JEAN-PAUL  
; TITLE OF INVENTION: CYTOTOXIC T LYMPHOCYTE

Query Match 14.6%; Score 39; DB 3; Length 36;  
Best Local Similarity 37.5%; Pred. No. 1.6e+02;  
Matches 6; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 12 LYKEGDPAPYKNPERW 27  
:|:::| | | | |  
Db 5 MYRQNPVPVGNIRW 20

RESULT 22  
US-10-027-038-14  
; Sequence 14, Application US/10027038  
; Patent No. 6822073  
; GENERAL INFORMATION:  
; APPLICANT: Quirk, S.  
; TITLE OF INVENTION: Modular peptide-based reagent  
; FILE REFERENCE: 1443.026US1  
; CURRENT APPLICATION NUMBER: US/10/027,038  
; CURRENT FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14  
; LENGTH: 35  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: A peptide backbone.  
; US-10-027-038-14

Query Match 14.4%; Score 38.5; DB 4; Length 35;  
Best Local Similarity 34.4%; Pred. No. 1.8e+02;



Matches 11; Conservative 2; Mismatches 6; Indels 13; Gaps 2;

Qy 16 GDPAP-----YKNPERWYRASPPITVTAA 40  
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Db 9 GDPGVEDLIRFYDNLQWLNC-----VTAA 34

RESULT 23  
US-10-027-038-11  
; Sequence 11, Application US/10027038  
; Patent No. 6822073  
; GENERAL INFORMATION:  
; APPLICANT: Quirk, S.  
; TITLE OF INVENTION: Modular peptide-based reagent  
; FILE REFERENCE: 1443.026US1  
; CURRENT APPLICATION NUMBER: US/10/027,038  
; CURRENT FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: A peptide backbone.  
US-10-027-038-11

Query Match 14.4%; Score 38.5; DB 4; Length 36;  
Best Local Similarity 34.4%; Pred. No. 1.9e+02;  
Matches 11; Conservative 2; Mismatches 6; Indels 13; Gaps 2;

Qy 16 GDPAP-----YKNPERWYRASPPITVTAA 40  
| | | | | : | | | |  
Db 10 GDPGVEDLIRFYDNLQWLNC-----VTAA 35

RESULT 24  
US-09-763-331-7  
; Sequence 7, Application US/09763331  
; Patent No. 6825335  
; GENERAL INFORMATION:  
; APPLICANT: Martin, Charles E.  
; APPLICANT: Mitchell, Andrew  
; TITLE OF INVENTION: Synthetic Fatty Acid Desaturase Gene for  
; TITLE OF INVENTION: Expression in Plants  
; FILE REFERENCE: 97-0081 PCT  
; CURRENT APPLICATION NUMBER: US/09/763,331  
; CURRENT FILING DATE: 1999-08-24  
; PRIOR APPLICATION NUMBER: US 60/097,586  
; PRIOR FILING DATE: 1998-08-24  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 33  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-09-763-331-7

Query Match 14.2%; Score 38; DB 4; Length 33;  
Best Local Similarity 30.8%; Pred. No. 2e+02;  
Matches 8; Conservative 3; Mismatches 7; Indels 8; Gaps 1;

Qy 11 ALYKEGDPAPYKNPER-----WY 28  
| : | | | | | | | |  
Db 4 ANYREAKECIYVEPDREGDKGVWY 29

RESULT 25  
US-08-332-562A-27  
; Sequence 27, Application US/08332562A  
; Patent No. 5985599  
; GENERAL INFORMATION:  
; APPLICANT: MCKENZIE, Ian F.C.

APPLICANT: HOGARTH, Mark P.  
APPLICANT: HIBBS, Margaret L.  
APPLICANT: SCOTT, Bernadette M.  
APPLICANT: BONADONNA, Lisa  
APPLICANT: HULETT, Mark D.  
TITLE OF INVENTION: PC RECEPTOR FOR IMMUNOGLOBULIN  
NUMBER OF SEQUENCES: 136  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/332,562A  
FILING DATE: 31-OCT-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/896,457  
FILING DATE: 27-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 54270/119/GRHA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-332-562A-27

Query Match 14.2%; Score 38; DB 2; Length 45;  
Best Local Similarity 41.2%; Pred. No. 2.9e+02;  
Matches 7; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 31 SFPITVTAAHSGTYRC 47  
| : | | | | | | | |  
Db 29 TFSIPQANHSHSGDYHC 45

Search completed: October 29, 2005, 04:28:36  
Job time : 44 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 29, 2005, 04:25:07 ; Search time 165 Seconds

(without alignments)  
119.079 Million cell updates/sec

Title: US-09-503-387-3\_COPY\_134\_180

Perfect score: 268

Sequence: 1 CQRYGDFQFALYKEGDPAP.....YRASFPITVTAAHSCTYRC 47

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Gapop 10.0 , Gapext 0.5

Searched: 1865214 seqs, 418043040 residues

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Minimum DB seq length: 0

Maximum DB seq length: 48

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA.\*

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22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	268	100.0	47	9	US-09-832-312-7
2	268	100.0	47	11	US-09-829-495-7
3	268	100.0	47	16	US-10-850-034-7
4	220	82.1	47	9	US-09-832-312-23
5	220	82.1	47	11	US-09-829-495-23
6	220	82.1	47	16	US-10-850-034-23
7	47	17.5	45	15	US-10-424-599-152673
8	46.5	17.4	26	15	US-10-403-847-143
9	46.5	17.4	34	14	US-10-040-862-9616
10	46.5	17.4	34	15	US-10-057-475B-9616
11	46.5	17.4	34	15	US-10-154-884B-9616

12	46.5	17.4	34	16	US-10-764-324-9616	Sequence 9616, Ap
13	46	17.2	32	16	US-10-425-115-325445	Sequence 325445,
14	45.5	17.0	44	14	US-10-321-857-60	Sequence 60, Appl
15	45.5	17.0	44	14	US-10-318-675-60	Sequence 60, Appl
16	45	16.8	44	17	US-10-477-525-15	Sequence 15, Appl
17	45	16.8	30	14	US-10-040-862-10445	Sequence 10445, A
18	45	16.8	30	15	US-10-057-475B-10445	Sequence 10445, A
19	45	16.8	30	15	US-10-154-884B-10445	Sequence 10445, A
20	45	16.8	30	16	US-10-764-324-10445	Sequence 10445, A
21	45	16.8	41	15	US-10-154-884B-11154	Sequence 11154, A
22	45	16.8	43	15	US-10-424-599-179261	Sequence 179261,
23	44.5	16.6	45	9	US-09-764-869-997	Sequence 997, App
24	44.5	16.6	45	14	US-10-091-504-997	Sequence 997, App
25	44.5	16.6	45	15	US-10-227-577-997	Sequence 997, App
26	44.5	16.6	45	16	US-10-425-115-195108	Sequence 195108,
27	44	16.4	34	15	US-10-424-599-173732	Sequence 173732,
28	44	16.4	42	9	US-09-731-449-21	Sequence 21, Appl
29	44	16.4	42	14	US-10-254-426-21	Sequence 21, Appl
30	44	16.4	46	16	US-10-425-115-348493	Sequence 348493,
31	44	16.4	47	9	US-09-731-449-23	Sequence 22, Appl
32	44	16.4	47	9	US-09-731-449-23	Sequence 23, Appl
33	44	16.4	47	13	US-10-105-934-17	Sequence 17, Appl
34	44	16.4	47	14	US-10-254-426-22	Sequence 22, Appl
35	44	16.4	47	14	US-10-254-426-23	Sequence 23, Appl
36	44	16.4	47	17	US-10-895-676-17	Sequence 17, Appl
37	43	16.0	13	15	US-10-462-452-374	Sequence 374, App
38	43	16.0	13	15	US-10-462-452-390	Sequence 390, App
39	43	16.0	13	15	US-10-601-953-502	Sequence 502, App
40	43	16.0	13	15	US-10-601-953-518	Sequence 518, App
41	43	16.0	13	16	US-10-322-266-375	Sequence 375, App
42	43	16.0	13	16	US-10-322-266-376	Sequence 376, App
43	43	16.0	13	16	US-10-322-266-391	Sequence 391, App
44	43	16.0	14	15	US-10-462-452-375	Sequence 375, App
45	43	16.0	14	15	US-10-462-452-391	Sequence 391, App
46	43	16.0	14	15	US-10-601-953-503	Sequence 503, App
47	43	16.0	14	15	US-10-601-953-519	Sequence 519, App
48	43	16.0	14	16	US-10-322-266-392	Sequence 392, App
49	43	16.0	17	15	US-10-462-452-369	Sequence 369, App
50	43	16.0	17	15	US-10-462-452-385	Sequence 385, App
51	43	16.0	17	15	US-10-601-953-497	Sequence 497, App
52	43	16.0	17	15	US-10-601-953-513	Sequence 513, App
53	43	16.0	17	16	US-10-322-266-370	Sequence 370, App
54	43	16.0	17	16	US-10-322-266-386	Sequence 386, App
55	43	16.0	19	15	US-10-462-452-370	Sequence 370, App
56	43	16.0	19	15	US-10-462-452-386	Sequence 386, App
57	43	16.0	19	15	US-10-601-953-498	Sequence 498, App
58	43	16.0	19	15	US-10-601-953-514	Sequence 514, App
59	43	16.0	19	16	US-10-322-266-387	Sequence 387, App
60	43	16.0	30	15	US-10-057-475B-10834	Sequence 10834, A
61	43	16.0	30	15	US-10-154-884B-10834	Sequence 10834, A
62	43	16.0	39	15	US-10-424-599-255712	Sequence 255712,
63	43	16.0	39	15	US-09-832-312-22	Sequence 22, Appl
64	43	16.0	41	9	US-09-829-495-22	Sequence 22, Appl
65	43	16.0	41	11	US-10-850-034-22	Sequence 22, Appl
66	43	16.0	41	15	US-10-312-829-17	Sequence 17, Appl
67	42.5	15.9	21	15	US-10-312-829-17	Sequence 17, Appl
68	42	15.7	12	15	US-10-462-452-373	Sequence 373, App
69	42	15.7	12	15	US-10-462-452-389	Sequence 389, App
70	42	15.7	12	15	US-10-601-953-501	Sequence 501, App
71	42	15.7	12	15	US-10-601-953-517	Sequence 517, App
72	42	15.7	12	16	US-10-322-266-374	Sequence 374, App
73	42	15.7	12	16	US-10-322-266-390	Sequence 390, App
74	42	15.7	15	15	US-10-462-452-368	Sequence 368, App
75	42	15.7	15	15	US-10-462-452-384	Sequence 384, App
76	42	15.7	15	15	US-10-601-953-496	Sequence 496, App
77	42	15.7	15	15	US-10-601-953-512	Sequence 512, App
78	42	15.7	15	16	US-10-322-266-369	Sequence 369, App
79	42	15.7	15	16	US-10-322-266-385	Sequence 385, App
80	42	15.7	30	16	US-10-933-767-846	Sequence 846, App
81	42	15.7	30	14	US-10-004-860-646	Sequence 646, App
82	42	15.7	30	14	US-10-023-282-646	Sequence 646, App
83	42	15.7	47	16	US-10-425-115-282892	Sequence 282892,
84	41	15.3	16	15	US-10-403-847-111	Sequence 111, App

Sequence 491, App  
Sequence 34, Appl  
Sequence 57, Appl  
Sequence 256207,  
Sequence 33, Appl  
Sequence 36, Appl  
Sequence 40395, A  
Sequence 607, App  
Sequence 607, App  
Sequence 178387,  
Sequence 47178, A  
Sequence 438, App  
Sequence 454, App  
Sequence 439, App  
Sequence 455, App  
Sequence 107, App

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, PRIOR APPLICATION NUMBER: 09/503,387
, PRIOR FILING DATE: 2000-02-14
, PRIOR APPLICATION NUMBER: 09/454,824
, PRIOR FILING DATE: 1999-12-06
, PRIOR APPLICATION NUMBER: 09/345,468
, PRIOR FILING DATE: 1999-06-30
, NUMBER OF SEQ ID NOS: 78
, SOFTWARE: Fast-Seq for Windows Version 1.0
, SEQ ID NO 7
, LENGTH: 47
, TYPE: prt
, ORGANISM: Homo sapiens
US-09-829-495-7

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## ALIGNMENTS

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RESULT 1
US-09-832-312-7
; Sequence 7, Application US/09832312
; Patent No. US20010049829A1
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-312-7

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RESULT 2
US-09-829-495-7
; Sequence 7, Application US/09829495
; Publication No. US20040001826A1
; GENERAL INFORMATION:
; APPLICANT: Busfield SJ
; APPLICANT: Villaveal J
; APPLICANT: Jandrot-Perrus M
; APPLICANT: Vainchenker W
; APPLICANT: Gill DS
; APPLICANT: Qian MD
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/829,495
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30

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Query Match      100.0%; Score 268; DB 16; Length 47;
Best Local Similarity 100.0%; Pred. No. 1.le-26;
Matches 47; Conservative 0; Mismatches 0; Indels

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Db       1 CQRYGFDQFALYKGGDPAPYKPKPERWYRASFLIIITVTAHSGTYRC 47
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RESULT 4
US-09-832-312-23
; Sequence 23, Application US/09832312
; Patent No. US20010049829A1
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234

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RESULT 6  
US-10-850-034-23  
; Sequence 23, Application US/10850034  
; Publication No. US20040253236A1  
; GENERAL INFORMATION:  
; APPLICANT: Busfield SJ

OY  
9 QFA--LYKEGDPAPYNPERW-----YRASFPITVTAAHS 42

NH  
2 EFAMMIVLDGIQVVDNIHWCDLPDDCYAARDCEATSGHS 45

## RESULT 8

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US-10-403-847-143
; Sequence 143, Application US/10403847
; Publication No. US20040030098A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL TWO SPLICED VARIANTS OF A HUMAN
; FILE REFERENCE: D0228 NP
; CURRENT APPLICATION NUMBER: US/10/403,847
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: U.S. 60/368,671
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: U.S. 60/371,420
; PRIOR FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 143
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-847-143

Query Match      17.4%; Score 46.5; DB 15; Length 26;
Best Local Similarity 55.6%; Pred. No. 1.2e+02;
Matches 10; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

Qy      30 ASFFIITVTAHSGTYRC 47
Db      6 ASFN-LSLTAHSGNYSC 22
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      ||| :||| ||| |||

RESULT 9
US-10-040-862-9616
; Sequence 9616, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
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; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467

US-10-040-862-9616
; Sequence 9616, Application US/10057475B
; Publication No. US20040002068A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordonez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-014402US
; CURRENT APPLICATION NUMBER: US/10/057,475B
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10979
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9616
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-057-475B-9616

Query Match      17.4%; Score 46.5; DB 15; Length 34;
Best Local Similarity 55.6%; Pred. No. 1.6e+02;
Matches 10; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

Qy      30 ASFFIITVTAHSGTYRC 47
Db      12 ASFN-LSLTAHSGNYSC 28
      ||| :||| ||| |||
      ||| :||| ||| |||

US-10-057-475B-9616
; Sequence 9616, Application US/10057475B
; Publication No. US20040002068A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordonez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-014402US
; CURRENT APPLICATION NUMBER: US/10/057,475B
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10979
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9616
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-057-475B-9616

Query Match      17.4%; Score 46.5; DB 15; Length 34;
Best Local Similarity 55.6%; Pred. No. 1.6e+02;
Matches 10; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

Qy      30 ASFFIITVTAHSGTYRC 47
Db      12 ASFN-LSLTAHSGNYSC 28
      ||| :||| ||| |||
      ||| :||| ||| |||
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RESULT 11
US-10-154-884B-9616
; Sequence 9616, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9616
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-9616

Query Match      17.4%; Score 46.5; DB 15; Length 34;
Best Local Similarity 55.6%; Pred. No. 1.6e+02;
Matches 10; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

Qy      30 ASFPITVTAAHSGTYRC 47
Db      12 ASFN-LSLTAHSGNYSC 28

RESULT 12
US-10-154-884B-9616
; Sequence 9616, Application US/10764324
; Publication No. US20040175739A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/764,324
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: US/10/040,862
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
```

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; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9616
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-764-324-9616

Query Match      17.4%; Score 46.5; DB 16; Length 34;
Best Local Similarity 55.6%; Pred. No. 1.6e+02;
Matches 10; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

Qy      30 ASFPITVTAAHSGTYRC 47
Db      12 ASFN-LSLTAHSGNYSC 28

RESULT 13
US-10-425-115-325445
; Sequence 325445, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 325445
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(32)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MFT4577_59877C.1.pep
US-10-425-115-325445

Query Match      17.2%; Score 46; DB 16; Length 32;
Best Local Similarity 44.4%; Pred. No. 1.8e+02;
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy      18 PAPYKNPERWYRASPPII 35
Db      7 PPPAESPPYYRGRLPPII 24

RESULT 14
US-10-321-857-60
; Sequence 60, Application US/10321857
; Publication No. US20030180816A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Applied NanoSystems B.V.
; TITLE OF INVENTION: A method to provide bacterial ghosts with antigens
; FILE REFERENCE: 2183-5547US
; CURRENT APPLICATION NUMBER: US/10/321.857
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/NL02/00383
; PRIOR FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: 01202239.8
; PRIOR FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Pseudomonas putida
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(44)
; OTHER INFORMATION: AcmA cell wall binding domain homologue
US-10-321-857-60

Query Match      17.0%; Score 45.5; DB 14; Length 44;
Best Local Similarity 52.2%; Pred. No. 2.9e+02;
Matches 12; Conservative 1; Mismatches 1; Indels 9; Gaps 2;

QY      4 RYGFDPQFALYKE-----GDPAPY 21
      |||||
Db      15 RYGWD----YKELAAARNGIPAPY 33
      |||||

RESULT 15
US-10-318-675-60
; Sequence 60, Application US/10318675
; Publication No. US20030186851A1
; GENERAL INFORMATION:
; APPLICANT: Applied NanoSystems B.V.
; TITLE OF INVENTION: Bacterial ghosts provided with antigens
; FILE REFERENCE: 2183-5546US
; CURRENT APPLICATION NUMBER: US/10/318.675
; PRIOR FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: PCT/NL02/00383
; PRIOR FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: 01202239.8
; PRIOR FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Pseudomonas putida
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(44)
; OTHER INFORMATION: AcmA cell wall binding domain homologue
US-10-318-675-60

Query Match      17.0%; Score 45.5; DB 14; Length 44;
Best Local Similarity 52.2%; Pred. No. 2.9e+02;
Matches 12; Conservative 1; Mismatches 1; Indels 9; Gaps 2;

QY      4 RYGFDPQFALYKE-----GDPAPY 21
      |||||
Db      15 RYGWD----YKELAAARNGIPAPY 33
      |||||

RESULT 16
US-10-477-525-15
; Sequence 15, Application US/10477525
; Publication No. US20050107314A1
; GENERAL INFORMATION:
; APPLICANT: GORCZYNSKI, Reginald M.
; APPLICANT: MARSDEN, Philip
```

```
; TITLE OF INVENTION: Modulation of CD200 Receptors
; FILE REFERENCE: 9579-81
; CURRENT APPLICATION NUMBER: US/10/477,525
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 60/292,950
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/369,862
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CD200R1
US-10-477-525-15

Query Match      16.8%; Score 45; DB 17; Length 24;
Best Local Similarity 39.3%; Pred. No. 1.7e+02;
Matches 11; Conservative 1; Mismatches 10; Indels 6; Gaps 1;

QY      20 PYKNPWRWYRASFPFIITVTAHSGTYRC 47
      |||||
Db      3 PDHSPE-----LQISAVTLQHEGTYTC 24
      |||||

RESULT 17
US-10-040-862-10445
; Sequence 10445, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10445
; LENGTH: 30
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-10-040-862-10445

Query Match      16.8%; Score 45; DB 14; Length 30;
Best Local Similarity 53.8%; Pred. No. 2.2e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy      35 ITVTAHSGTYRC 47
Db      4 LSLTAHSGNYSC 16

RESULT 18
US-10-057-475B-10445
; Sequence 10445, Application US/10057475B
; Publication No. US20040002068A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordonez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-014402US
; CURRENT APPLICATION NUMBER: US/10/057,475B
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10979
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10445
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-057-475B-10445

Query Match      16.8%; Score 45; DB 15; Length 30;
Best Local Similarity 53.8%; Pred. No. 2.2e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy      35 ITVTAHSGTYRC 47
Db      4 LSLTAHSGNYSC 16

RESULT 19
US-10-154-884B-10445
; Sequence 10445, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/764,324
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: US/10/040,862
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
```

```
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10445
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-10445

Query Match      16.8%; Score 45; DB 15; Length 30;
Best Local Similarity 53.8%; Pred. No. 2.2e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy      35 ITVTAHSGTYRC 47
Db      4 LSLTAHSGNYSC 16

RESULT 20
US-10-764-324-10445
; Sequence 10445, Application US/10764324
; Publication No. US2004017539A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/764,324
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: US/10/040,862
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
```



```

US-10-227-577-997

Query Match          16.6%; Score 44.5; DB 15; Length 45;
Best Local Similarity 38.5%; Pred. NO. 4e+02;
Matches 15; Conservative 1; Mismatches 12; Indels 1

Qy 9 QFALYKEGDPAKYKPERWYRASFPILITTAHAHSCTYRC 47
      |||||      |||||      |||||
Db 1 QFLDLKLG-----MWTASIPLI--TGVHSGKNRC 28

Search completed: October 29, 2005, 04:41:11
Job time : 166 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 29, 2005, 04:08:36 ; Search time 38 Seconds

(without alignments)  
119.005 Million cell updates/sec

Title: US-09-503-387-3\_COPY\_134\_180

Perfect score: 268

Sequence: 1 CQTRYGDFQFALYKEGPAP.....YRASFPITVTAAHSGTYRC 47

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 11254

Minimum DB seq length: 0

Maximum DB seq length: 48

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : PIR 79:\*

1: Pirl:\*

2: Pirl:\*

3: Pirl:\*

4: Pirl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	13.8	29	2 S10061	Ig heavy chain (cl
2	36	13.4	43	2 B42057	fibroblast growth
3	36	13.4	47	2 A41266	fibroblast growth
4	35.5	13.2	34	2 S65716	prostaglandin-D sy
5	35	13.1	24	2 T42256	protein phosphatas
6	35	13.1	30	2 D70144	hypothetical prote
7	35	13.1	36	2 S07052	neuropeptide Y - s
8	35	13.1	38	2 PL0229	T-cell receptor be
9	35	13.1	46	2 D84334	hypothetical prote
10	34	12.7	20	2 T50757	pufK protein limpo
11	34	12.7	33	2 H81220	hypothetical prote
12	33	12.3	27	2 PN0586	tyrosine 3-monoxy
13	33	12.3	35	2 E38601	Ig kappa chain V r
14	33	12.3	35	2 AE0612	hypothetical prote
15	33	12.3	36	2 A28578	pancreatic hormone
16	33	12.3	38	2 G45095	photosystem I ligh
17	33	12.3	39	2 S00490	RNA-binding protei
18	33	12.3	44	2 F85701	hypothetical prote
19	33	12.3	44	2 G85701	hypothetical prote
20	32.5	12.1	31	2 T48290	hypothetical prote
21	32.5	12.1	38	2 S40096	chlorophyll a/b-bi
22	32.5	12.1	42	4 JE00021	probable 4.8K prot
23	32.5	12.1	44	2 AD1753	Lactococcus lactis
24	32.5	12.1	46	2 PC1066	antimorphine pepti
25	32	11.9	20	2 S18582	hypothetical prote
26	32	11.9	24	2 A60556	cytochrome c552 -
27	32	11.9	24	2 S35641	DNA (cytosine-5-)-
28	32	11.9	30	2 S20778	Ig heavy chain V r
29	32	11.9	36	2 A30485	neuropeptide Y - r

30	32	11.9	36	2 B30485	neuropeptide Y - g
31	32	11.9	36	2 S00317	photosystem I lik
32	32	11.9	41	2 G70214	hypothetical prote
33	32	11.9	42	2 S20767	Ig heavy chain V r
34	32	11.9	43	2 A43616	actin alpha, cardi
35	31.5	11.8	29	2 B81006	hypothetical prote
36	31.5	11.8	35	2 S13435	lectin III - furze
37	31	11.6	11	2 D61033	ranatachykinin D -
38	31	11.6	29	2 S58388	T-cell receptor be
39	31	11.6	30	2 S60336	phosphatidylinosit
40	31	11.6	31	2 T01701	hypothetical prote
41	31	11.6	34	2 S36843	defensin NP-6 - ra
42	31	11.6	34	2 F82163	hypothetical prote
43	31	11.6	36	1 NYPGY	neuropeptide Y - p
44	31	11.6	37	2 C83780	hypothetical prote
45	31	11.6	39	2 J70620	glutamate dehydrog
46	31	11.6	39	2 S20769	Ig heavy chain V r
47	31	11.6	39	2 I51219	adrenergic recepto
48	31	11.6	40	2 A40128	probable antigen 1
49	31	11.6	41	2 PQ0104	microbial serine p
50	31	11.6	45	2 B47187	phosphoprotein pho
51	31	11.6	47	2 J70518	Ig heavy chain V-I
52	31	11.6	47	2 A81730	hypothetical prote
53	30.5	11.4	35	2 C44918	lactococcin G pept
54	30.5	11.4	40	2 S56006	takaracetin alpha
55	30.5	11.4	40	2 T07560	hypothetical prote
56	30.5	11.4	41	2 B27579	T-cell receptor be
57	30.5	11.4	42	2 B82770	hypothetical prote
58	30.5	11.4	45	2 B97484	hypothetical prote
59	30	11.2	10	2 F49033	T-cell receptor ga
60	30	11.2	21	2 PQ0145	glucan endo-1,3-be
61	30	11.2	25	2 I51151	alpha actin - quai
62	30	11.2	30	2 C32946	serine proteinase
63	30	11.2	33	2 PH1743	Ig heavy chain V r
64	30	11.2	35	2 I55263	alpha-smooth muscl
65	30	11.2	35	2 I64003	hypothetical prote
66	30	11.2	35	2 A85660	hypothetical prote
67	30	11.2	37	2 A36440	NADH2 peroxidase (
68	30	11.2	37	2 G82814	hypothetical prote
69	30	11.2	38	2 T01677	pseudo-kallikrein
70	30	11.2	38	2 B24376	trypsin inhibitor
71	30	11.2	38	2 A49040	T-cell receptor be
72	30	11.2	38	2 A44862	microtubule associ
73	30	11.2	41	2 F95098	hypothetical prote
74	30	11.2	45	1 RUDVD	rubredoxin [valida
75	30	11.2	46	2 A10624	probable DNA inver
76	30	11.2	46	2 C83437	hypothetical prote
77	30	11.2	48	2 D83898	hypothetical prote
78	29	10.8	14	2 PH0792	T-cell receptor al
79	29	10.8	17	2 S57991	hydroxyproline-ric
80	29	10.8	18	2 A59137	protein P11 - gold
81	29	10.8	19	2 A41668	integrin alpha-7 c
82	29	10.8	20	2 A36045	thrombospondin hom
83	29	10.8	22	2 B32946	serine proteinase
84	29	10.8	24	2 S65714	lectin GNL alpha c
85	29	10.8	27	2 PH1720	Ig heavy chain V r
86	29	10.8	29	2 D32533	class II histocomp
87	29	10.8	30	2 H81202	hypothetical prote
88	29	10.8	32	2 PC4433	paired box transcr
89	29	10.8	33	2 PC4435	H-2 class I histoc
90	29	10.8	34	2 PS0137	hypothetical prote
91	29	10.8	35	2 F84395	29K antigen PB2 -
92	29	10.8	35	2 B41161	neuropeptide Y - l
93	29	10.8	36	2 A39393	neuropeptide Y - c
94	29	10.8	36	2 A48540	actin 1 - mouse (f
95	29	10.8	36	2 PN0041	Tla class I histoc
96	29	10.8	37	2 B45875	glutathione transf
97	29	10.8	42	2 S29098	hypothetical prote
98	29	10.8	43	2 B97155	Ig heavy chain V r
99	29	10.8	45	2 S20776	GTP cyclohydrolase
100	29	10.8	46	2 I39904	

## ALIGNMENTS

```
RESULT 1
S10061
IG heavy chain (clone J12) - African clawed frog (fragment)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 21-Nov-1993 #sequence_revision 08-Nov-1996 #text_change 15-Oct-1999
C;Accession: S10061; E49021
R;Schwager, J.; Grossberger, D.; du Pasquier, L.
EMBO J. 7, 2409-2415, 1988
A;Title: Organization and rearrangement of immunoglobulin M genes in the amphibian Xenopus
A;Reference number: S01158; MUID:89052653; PMID:2903824
A;Accession: S10061
A;Molecule type: mRNA
A;Residues: 1-29 <SCH>
A;Cross-references: EMBL:X14925; NID:g64844; PIDN:CAA33052.1; PID:g930274
A;Note: the authors translated the codon AAG for residue 5 as Leu and GAG for residue 8
R;Haire, R.N.; Amemiya, C.I.; Suzuki, D.; Litman, G.W.
J. Exp. Med. 171, 1721-1737, 1990
A;Title: Eleven distinct V-H gene families and additional patterns of sequence variation
A;Reference number: A47624; MUID:90237760; PMID:2110243
A;Accession: B49021
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 10-24 <HAI>
A;Note: J8 region
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;1-24/Domain: V-D-J region (fragment) #status predicted <VR>
F;25-29/Domain: C region (mu chain) (fragment) #status predicted <CRE>

Query Match      13.8%; Score 37; DB 2; Length 29;
Best Local Similarity 38.5%; Pred. No. 4.2e+02;
Matches 10; Conservative 5; Mismatches 9; Indels 2; Gaps 1;

Qy 19 APYKNPWRWR--ASFPIITVTAHS 42
      ||| |||:: :|||::|
Db 2 ARYKGVRYFHHWGQGTMTVTTSATS 27

RESULT 2
B42057
fibroblast growth factor receptor 1, membrane-bound - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: B42057
R;Werner, S.; Duan, D.S.R.; de Vries, C.; Peters, K.G.; Johnson, D.E.; Williams, L.T.
Mol. Cell. Biol. 12, 82-88, 1992
A;Title: Differential splicing in the extracellular region of fibroblast growth factor r
A;Reference number: A42057; MUID:92107200; PMID:1309595
A;Accession: B42057
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-43 <WER>
A;Cross-references: UNIPROT:Q9QUJ17; UNIPROT:Q9QZM7; GB:M80363
C;Keywords: growth factor receptor; membrane protein

Query Match      13.4%; Score 36; DB 2; Length 43;
Best Local Similarity 50.0%; Pred. No. 8.4e+02;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 34 IITVTAHSGTYRC 47
      : ||| ||| ||
Db 13 LPNVTEAQSGEYVC 26

RESULT 3
A41266
fibroblast growth factor receptor 1, membrane-bound - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 09-Jul-2004
C;Accession: A41266
```

```
R;Johnson, D.E.; Lu, J.; Chen, H.; Werner, S.; Williams, L.T.
Mol. Cell. Biol. 11, 4627-4634, 1991
A;Title: The human fibroblast growth factor receptor genes: a common structural arrange
A;Reference number: A41266; MUID:91342665; PMID:1652059
A;Accession: A41266
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-47 <JOH>
A;Cross-references: UNIPROT:Q9UDF1
C;Keywords: growth factor receptor; membrane protein

Query Match      13.4%; Score 36; DB 2; Length 47;
Best Local Similarity 50.0%; Pred. No. 9.2e+02;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 34 IITVTAHSGTYRC 47
      : ||| ||| ||
Db 14 LPNVTEAQSGEYVC 27

RESULT 4
S65716
prostaglandin-D synthase (EC 5.3.99.2) - human (fragments)
N;Alternate names: prostaglandin-H2 D-isomerase
C;Species: Homo sapiens (man)
C;Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 09-May-1997
C;Accession: S65716
R;Giacomelli, S.; Leone, M.G.; Grima, J.; Silvestrini, B.; Cheng, C.Y.
Biochim. Biophys. Acta 1310, 269-276, 1996
A;Title: Astrocytes synthesize and secrete prostaglandin D synthetase in vitro.
A;Reference number: S65716; MUID:96177373; PMID:8599604
A;Accession: S65716
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-16;17-34 <GIA>
C;Superfamily: lipocalin; lipocalin homology
C;Keywords: intramolecular oxidoreductase; isomerase

Query Match      13.2%; Score 35.5; DB 2; Length 34;
Best Local Similarity 46.7%; Pred. No. 7.6e+02;
Matches 7; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

Qy 7 FDQFA-LYKEGDPA 20
      :|||: |||:|
Db 19 YDQYALLYSGSKGP 33

RESULT 5
T42256
protein phosphatase X - Caenorhabditis elegans (fragment)
C;Species: Caenorhabditis elegans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T42256
R;Zeke, T.; Gergely, P.; Dombradi, V.
submitted to the EMBL Data Library, July 1996
A;Description: The catalytic subunits of Ser/Thr protein phosphatases from Caenorhabditis
A;Reference number: Z22131
A;Accession: T42256
A;Status: preliminary; translated from GE/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-24 <ZEK>
A;Cross-references: UNIPROT:Q94375; EMBL:Z77736; PIDN:CAB01295.1
C;Genetics:
A;Note: PPX
C;Superfamily: serine/threonine protein phosphatase; phosphoesterase core homology; phosph

Query Match      13.1%; Score 35; DB 2; Length 24;
Best Local Similarity 35.3%; Pred. No. 6.2e+02;
Matches 6; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 7 FDQFALYKEGDPAFYKN 23
      :|||: |||:|
Db 3 YDLMELFRVGGPVNTN 19
```

A;Residues: 1-38 <LI>  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: T-cell receptor

Query Match 13.1%; Score 35; DB 2; Length 38;  
Best Local Similarity 40.0%; Pred. No. 9.9e+02;  
Matches 6; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 9 QFALYKGDPAKYKN 23  
DB 23 EFLYFQNSAPDKS 37

## RESULT 9

DB4334

hypothetical protein vngl832h [imported] - Halobacterium sp. NRC-1

C;Species: Halobacterium sp. NRC-1

C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004

C;Accession: DB4334

R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.;  
Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablon  
Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li  
A;Title: Genome sequence of Halobacterium species NRC-1.

A;Reference number: A84160; MUID:20504483; PMID:11016950

A;Accession: DB4334

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-46 <STO>

A;Cross-references: UNIPROT:Q9HP30; GB:AE004437; NID:g10581278; PIDN:AAG50040.1; GSPDB:G

C;Genetics:

A;Gene: VNG1832H

Query Match 13.1%; Score 35; DB 2; Length 46;  
Best Local Similarity 50.0%; Pred. No. 1.2e+03;  
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 18 PAPYKNPERWYRAS 31  
DB 12 PAATNRNDTRGYRSS 25

## RESULT 10

TS0757

pufK protein [imported] - Rhodobacter sphaeroides

C;Species: Rhodobacter sphaeroides

C;Date: 21-Jul-2000 #sequence\_revision 21-Jul-2000 #text\_change 09-Jul-2004

C;Accession: TS0757

R;Choudhary, M.; Kaplan, S.

Nucleic Acids Res. 28, 862-867, 2000

A;Title: DNA sequence analysis of the photosynthesis region of Rhodobacter sphaeroides 2.  
A;Reference number: Z25222; MUID:20115911; PMID:10648776

A;Accession: TS0757

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-20 <CHO>

A;Cross-references: UNIPROT:Q53121; EMBL:AF195122; PIDN:AAF24301.1

A;Experimental source: strain 2.4.1

C;Genetics:

A;Gene: pufK

Query Match 12.7%; Score 34; DB 2; Length 20;  
Best Local Similarity 50.0%; Pred. No. 6.8e+02;  
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 20 PYKNPERWYRAS 31  
DB 3 PYKNPRHORVAS 14

## RESULT 11

H81220

## RESULT 6

D70144

hypothetical protein BB0357 - Lyme disease spirochete

C;Species: Borrelia burgdorferi (Lyme disease spirochete)

C;Date: 13-Feb-1998 #sequence\_revision 13-Feb-1998 #text\_change 09-Jul-2004

C;Accession: D70144

R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White  
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,  
Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.  
Nature 390, 580-586, 1997

A;Authors: Smith, H.O.; Venter, J.C.

A;Title: Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.

A;Reference number: A70100; MUID:98065943; PMID:9403685

A;Accession: D70144

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-30 <KLE>

A;Cross-references: UNIPROT:O51332; GB:AE001141; GB:AE000783; NID:g2688250; PIDN:AAC6673  
A;Experimental source: strain B31

Query Match 13.1%; Score 35; DB 2; Length 30;  
Best Local Similarity 42.9%; Pred. No. 7.8e+02;  
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 21 YKNPERWTRASPPI 34

DB 8 YSKPDRFYFLGVPI 21

## RESULT 7

S07052

neuropeptide Y - sheep

C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C;Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004

C;Accession: S07052

R;Sillard, R.; Agerberth, B.; Mutt, V.; Joernvall, H.

FEBS Lett. 258, 263-265, 1989

A;Title: Sheep neuropeptide Y. A third structural type of a highly conserved peptide.

A;Reference number: S07052; MUID:90092485; PMID:2595092

A;Accession: S07052

A;Molecule type: protein

A;Residues: 1-36 <SIL>

A;Cross-references: UNIPROT:P14765

C;Function:

A;Description: neuropeptide inducing a number of behavioral effects including stimulat

C;Superfamily: pancreatic hormone

C;Keywords: amidated carboxyl end; appetite; hormone; neuropeptide

F1-36/Product: neuropeptide Y #status experimental <MAT>

F1-36/Modified site: amidated carboxyl end (Tyr) #status experimental

Query Match 13.1%; Score 35; DB 2; Length 36;

Best Local Similarity 46.7%; Pred. No. 9.4e+02;

Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 16 GDPAPYKNPERWYRA 30

DB 9 GDDAPAEIDLARYSA 23

## RESULT 8

PL0229

T-cell receptor beta chain V region (V-beta-6.7a, PCR-2) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 30-May-1997

C;Accession: PL0229

R;Li, Y.; Szabo, P.; Robinson, M.A.; Dong, B.; Pennett, D.N.

J. Exp. Med. 171, 221-230, 1990

A;Title: Allelic variations in the human T cell receptor V-beta-6.7 gene products.

A;Reference number: PL0229; MUID:90111615; PMID:1967299

A;Accession: PL0229

A;Molecule type: mRNA

RESULT 16  
G45095  
photosystem I light-harvesting complex chlorophyll a/b protein p22.1/p22 - Chlamydomonas



C:Species: Chlamydomonas reinhardtii  
 C:Date: 30-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
 C:Accession: G45095  
 R:Baasi, R.; Soen, S.Y.; Frank, G.; Zuber, H.; Roehaix, J.D.  
 J. Biol. Chem. 267, 25714-25721, 1992  
 A:Title: Characterization of chlorophyll a/b proteins of photosystem I from Chlamydomonas  
 A:Reference number: A45095; MUID:93100280; PMID:1464588  
 A:Accession: G45095  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-38 <BAS>  
 A:Cross-references: UNIPROT:Q9S0T9  
 A:Note: sequence extracted from NCBI backbone (NCBIP:120940)  
 C:Superfamily: chlorophyll a/b-binding protein  
 C:Keywords: chloroplast; thylakoid

Query Match 12.3%; Score 33; DB 2; Length 38;  
 Best Local Similarity 52.6%; Pred. No. 1.8e+03;  
 Matches 10; Conservative 1; Mismatches 4; Indels 2;

QY 5 YGDFQFALYKED-PAPYK 22  
 ||||| : |||||  
 DB 23 YGDFPLSL---GDEPASLK 38

RESULT 17  
 S00490  
 RNA-binding protein, 62K - rabbit (tentative sequence) (fragment)  
 C:Species: Oryctolagus cuniculus (domestic rabbit)  
 C:Date: 31-Dec-1988 #sequence\_revision 31-Dec-1990 #text\_change 09-Jul-2004  
 C:Accession: S00490  
 R:Slobin, L.I.; Greenberg, J.R.  
 Eur. J. Biochem. 173, 305-310, 1988  
 A:Title: Purification and properties of a protein component of messenger ribonucleoprotein  
 A:Reference number: S00490; MUID:88196114; PMID:2452088  
 A:Accession: S00490  
 A:Molecule type: protein  
 A:Residues: 1-39 <SLO>  
 A:Cross-references: UNIPROT:P13642  
 C:Comment: This protein binds to both messenger and ribosomal RNA.  
 C:Superfamily: serine-tRNA ligase  
 C:Keywords: RNA binding

Query Match 12.3%; Score 33; DB 2; Length 39;  
 Best Local Similarity 58.3%; Pred. No. 1.8e+03;  
 Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 8 DQFALYKGDPA 19  
 ||||| : |||||  
 DB 5 DLFRVDKGDPA 16

RESULT 18  
 F85701  
 hypothetical protein Z1987 [imported] - Escherichia coli (strain O157:H7, substrain EDL93)  
 C:Species: Escherichia coli  
 C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004  
 C:Accession: F85701  
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew,  
 Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,  
 Nature 409, 529-533, 2001  
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
 A:Reference number: A85480; MUID:21074935; PMID:11206551  
 A:Accession: F85701  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-44 <STO>  
 A:Cross-references: UNIPROT:Q8X416; GB:AE005174; NID:g12514932; PIDN:AAG56074.1; GSPDB:G  
 A:Experimental source: strain O157:H7, substrain EDL933  
 C:Genetics:  
 A:Gene: Z1987

Query Match 12.3%; Score 33; DB 2; Length 44;

Best Local Similarity 36.4%; Pred. No. 2.1e+03;  
 Matches 8; Conservative 5; Mismatches 7; Indels 2; Gaps 1;

QY 27 WYRASFPPIIT--VTAHSGTYR 46  
 : : ||| : ||| : |||  
 DB 20 WHDLAAPILAGITTAIVGWWR 41

RESULT 19  
 G85701  
 hypothetical protein Z1989 [imported] - Escherichia coli (strain O157:H7, substrain EDL93)  
 C:Species: Escherichia coli  
 C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004  
 C:Accession: G85701  
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew,  
 Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,  
 Nature 409, 529-533, 2001  
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
 A:Reference number: A85480; MUID:21074935; PMID:11206551  
 A:Accession: G85701  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-44 <STO>  
 A:Cross-references: UNIPROT:Q8X415; GB:AE005174; NID:g12514933; PIDN:AAG56075.1; GSPDB:G  
 A:Experimental source: strain O157:H7, substrain EDL933  
 C:Genetics:  
 A:Gene: Z1989

Query Match 12.3%; Score 33; DB 2; Length 44;  
 Best Local Similarity 36.4%; Pred. No. 2.1e+03;  
 Matches 8; Conservative 5; Mismatches 7; Indels 2; Gaps 1;

QY 27 WYRASFPPIIT--VTAHSGTYR 46  
 : : ||| : ||| : |||  
 DB 20 WHDLAAPILAGITTAIVGWWR 41

RESULT 20  
 T48290  
 hypothetical protein T22P11.280 - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004  
 C:Accession: T48290  
 R:Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft,  
 submitted to the Protein Sequence Database, April 2000  
 A:Reference number: Z24490  
 A:Accession: T48290  
 A:Molecule type: DNA  
 A:Residues: 1-31 <BEV>  
 A:Cross-references: UNIPROT:Q9LZ33; EMBL:AL162971  
 A:Experimental source: cultivar Columbia; BAC clone T22P11  
 C:Genetics:  
 A:Map position: 5  
 A:Introns: 26/2  
 A:Note: T22P11.280

Query Match 12.1%; Score 32.5; DB 2; Length 31;  
 Best Local Similarity 34.8%; Pred. No. 1.7e+03;  
 Matches 8; Conservative 4; Mismatches 10; Indels 1; Gaps 1;

QY 10 FALYKGDPA-PYKNPERWYRAS 31  
 : : ||| : ||| : |||  
 DB 8 FKQSKDDSSGSGFKYKELWYLS 30

RESULT 21  
 S40096  
 chlorophyll a/b-binding protein - moss (Physcomitrella patens)  
 C:Species: Physcomitrella patens  
 C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
 C:Accession: S40096  
 R:Reski, R.; Faust, M.; Wang, X.H.; Wehe, M.; Abel, W.O.

```
Matches 10; Conservative 3; Mismatches 12; Indels 1; Gaps 1;

QY      8 DQFALYKEG-DPAPYKNPERWYRAS F 32
          ||| : | : | : | : |
Db       16 DYFAEYEAAQNPNKKKARRASQADF 41

RESULT 24
PC1066
antimorphine peptide 60a - dog (fragment)
C/Species: Canis lupus familiaris (dog)
C/Date: 27-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C/Accession: PC1066
R/Liao, Z.R.; Zhang, S.N.; Wang, J.Y.; Chen, Y.Z.; Zhou, S.
Acta Sci. Natur. Univ. Pekin. 29, 680-686, 1993
A/Title: The isolation, purification, sequence of an antimorphine peptide (60a) from dog
A/Reference number: PC1066
A/Accession: PC1066
A/Molecule type: protein
A/Residues: 1-46 <LIA>
A/Cross-references: UNIPROT:Q7M391
A/Experimental source: brain
C/Comment: This peptide has a significant anti-morphine activity when intraventricularly
C/Keywords: brain

Query Match           12.1%; Score 32.5; DB 2; Length 46;
Best Local Similarity 41.2%; Pred. No. 2.5e+03;
Matches 7; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

QY      18 PAPY-KNPERWYRASFP 33
          ||| : | : | : |
Db       23 PAKYKGHPVHWFVIWWP 39

RESULT 25
SI8582
hypothetical protein K (pufQ 3' region) - Rhodobacter sphaeroides
C/Species: Rhodobacter sphaeroides
C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 03-May-1994
C/Accession: SI8582; S32855
R/Hunter, C.N.; McGlynn, P.; Ashby, M.K.; Burgess, J.G.; Olsen, J.D.
Mol. Microbiol. 5, 2649-2661, 1991
A/Title: DNA sequencing and complementation/deletion analysis of the bchA-puf operon reg
A/Reference number: SI8580; MUID:92140030; PMID:1779756
A/Accession: SI8582
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-20 <HUN>
A/Cross-references: EMBL:X68795

Query Match           11.9%; Score 32; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      20 PYKNPERWYRAS 31
          ||| : | : |
Db       3 PYRNPRNHVAS 14

Search completed: October 29, 2005, 04:24:51
Job time : 43 secs
```

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 29, 2005, 04:16:51 ; Search time 174 Seconds  
(without alignments)  
138.320 Million cell updates/sec

Title: US-09-503-387-3\_COPY\_134\_180

Perfect score: 268

Sequence: 1 CQRYGDFQFALYKEGPAP.....YRASFPPIITVAHSGTYRC 47

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 64033

Minimum DB seq length: 0  
Maximum DB seq length: 48

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : UniProt\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	16.4	48	2	Q8AFG1 mouse mamma
2	42	15.7	40	2	Q8EZ89 leptospira
3	41	15.3	25	2	Q93LX3 vibrio chol
4	41	15.3	35	2	Q8IRV5 bacillus an
5	41	15.3	42	2	Q7R533 giardia lam
6	41	15.3	47	2	Q7OU90 mycena pura
7	39	14.6	20	2	Q8NFW3 homo sapien
8	39	14.6	32	2	Q8UUN6 xenopus lae
9	39	14.6	33	2	O24624 pinus taeda
10	39	14.6	39	2	Q9HF16 epichloe am
11	39	14.6	39	2	Q9HF17 epichloe cf
12	39	14.6	41	2	O8JLH0 cryphonectr
13	39	14.6	46	2	Q8OB18 saimirine
14	39	14.6	46	2	Q8OBJ4 saimirine
15	39	14.6	46	2	Q8OBJ7 saimirine
16	39	14.6	46	2	Q8OBRS saimirine
17	39	14.6	47	2	Q6V8T8 malus domes
18	38	14.4	40	2	Q6U847 mycobacteri
19	38	14.2	28	2	Q7GLI0 pinus taeda
20	38	14.2	32	2	Q96W12 neotrophodi
21	38	14.2	33	2	O24637 pinus taeda
22	38	14.2	39	2	Q7LTM6 epichloe ty
23	38	14.2	39	2	Q7LTM7 epichloe ty
24	38	14.2	39	2	Q7LTM8 epichloe ty
25	38	14.2	39	2	Q7LTM9 epichloe ty
26	38	14.2	39	2	Q7LTM0 epichloe ty
27	38	14.2	39	2	Q7LTM1 epichloe ty
28	38	14.2	39	2	Q7LTM2 epichloe ty
29	38	14.2	39	2	Q7LTM3 epichloe ty
30	38	14.2	39	2	Q7LTM4 epichloe ty
31	38	14.2	39	2	Q7LTM5 epichloe ty

32	38	14.2	39	2	Q7LTN6	Q7ltm6 epichloe sy
33	38	14.2	39	2	Q7LTN7	Q7ltm7 epichloe gl
34	38	14.2	39	2	Q7LTN8	Q7ltm8 epichloe fe
35	38	14.2	39	2	Q7LTN9	Q7ltm9 epichloe fe
36	38	14.2	39	2	Q7LTP0	Q7ltm0 epichloe el
37	38	14.2	39	2	Q7LTP1	Q7ltm1 epichloe el
38	38	14.2	39	2	Q7LTP2	Q7ltm2 epichloe el
39	38	14.2	39	2	Q7LTP3	Q7ltm3 epichloe br
40	38	14.2	39	2	Q7LTP4	Q7ltm4 epichloe br
41	38	14.2	39	2	Q7LTP5	Q7ltm5 epichloe br
42	38	14.2	39	2	Q7LTP6	Q7ltm6 epichloe br
43	38	14.2	39	2	Q7LTP7	Q7ltm7 epichloe ba
44	38	14.2	39	2	Q9HDM2	Q9hdm2 epichloe ba
45	38	14.2	39	2	Q9HDM3	Q9hdm3 epichloe br
46	38	14.2	39	2	Q9HDM4	Q9hdm4 epichloe br
47	38	14.2	39	2	Q9HDM5	Q9hdm5 epichloe el
48	38	14.2	39	2	Q9HDM6	Q9hdm6 epichloe fe
49	38	14.2	39	2	Q9HDM7	Q9hdm7 epichloe gl
50	38	14.2	39	2	Q9HDM8	Q9hdm8 epichloe sy
51	38	14.2	39	2	Q9HDM9	Q9hdm9 epichloe ty
52	38	14.2	39	2	Q9HF13	Q9hfi13 epichloe ty
53	38	14.2	39	2	Q9HF14	Q9hfi14 epichloe cl
54	38	14.2	40	2	Q72F30	Q72f30 deulfovibr
55	38	14.2	45	2	Q95V78	Q95v78 bombyx mori
56	37.5	14.0	39	2	Q13254	Q13254 homo sapien
57	37	13.8	20	2	Q8X127	Q8x127 magnaporthe
58	37	13.8	20	2	Q8X128	Q8x128 magnaporthe
59	37	13.8	20	2	Q96VV9	Q96vv9 magnaporthe
60	37	13.8	20	2	Q96VW0	Q96vw0 magnaporthe
61	37	13.8	20	2	Q96VW1	Q96vw1 magnaporthe
62	37	13.8	20	2	Q96VW2	Q96vw2 magnaporthe
63	37	13.8	20	2	Q9C223	Q9c223 sclerotinia
64	37	13.8	20	2	Q9C224	Q9c224 sclerotinia
65	37	13.8	20	2	Q9C225	Q9c225 sclerotinia
66	37	13.8	20	2	Q9C226	Q9c226 sclerotinia
67	37	13.8	20	2	Q9C227	Q9c227 sclerotinia
68	37	13.8	20	2	Q9C228	Q9c228 sclerotinia
69	37	13.8	20	2	Q9C229	Q9c229 sclerotinia
70	37	13.8	20	2	Q9C300	Q9c300 sclerotinia
71	37	13.8	20	2	Q9C301	Q9c301 sclerotinia
72	37	13.8	20	2	Q9C302	Q9c302 sclerotinia
73	37	13.8	20	2	Q9C303	Q9c303 sclerotinia
74	37	13.8	20	2	Q9C304	Q9c304 sclerotinia
75	37	13.8	20	2	Q9C305	Q9c305 sclerotinia
76	37	13.8	20	2	Q9C306	Q9c306 sclerotinia
77	37	13.8	20	2	Q9C307	Q9c307 sclerotinia
78	37	13.8	20	2	Q9C308	Q9c308 sclerotinia
79	37	13.8	20	2	Q9C309	Q9c309 sclerotinia
80	37	13.8	20	2	Q9C310	Q9c310 sclerotinia
81	37	13.8	20	2	Q9C311	Q9c311 sclerotinia
82	37	13.8	20	2	Q9C312	Q9c312 sclerotinia
83	37	13.8	20	2	Q9C313	Q9c313 sclerotinia
84	37	13.8	20	2	Q9C314	Q9c314 sclerotinia
85	37	13.8	20	2	Q9C315	Q9c315 sclerotinia
86	37	13.8	20	2	Q9C316	Q9c316 sclerotinia
87	37	13.8	20	2	Q9C317	Q9c317 sclerotinia
88	37	13.8	20	2	Q9C318	Q9c318 sclerotinia
89	37	13.8	20	2	Q9C319	Q9c319 sclerotinia
90	37	13.8	20	2	Q9C320	Q9c320 sclerotinia
91	37	13.8	20	2	Q9C321	Q9c321 sclerotinia
92	37	13.8	20	2	Q9C322	Q9c322 sclerotinia
93	37	13.8	20	2	Q9C323	Q9c323 sclerotinia
94	37	13.8	20	2	Q9C324	Q9c324 sclerotinia
95	37	13.8	20	2	Q9C325	Q9c325 sclerotinia
96	37	13.8	20	2	Q9C326	Q9c326 sclerotinia
97	37	13.8	20	2	Q9C327	Q9c327 sclerotinia
98	37	13.8	20	2	Q9C328	Q9c328 sclerotinia
99	37	13.8	20	2	Q9C329	Q9c329 sclerotinia
100	37	13.8	20	2	Q9C330	Q9c330 sclerotinia

[illegible]

RT "Bacillus anthracis comparative genomics.";   
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.   
DR EMBL; AE017030; AAP25827.1; -   
DR EMBL; AE017334; AAT35319.1; -   
DR TIGR; BA1932; -   
DR TIGR; GBA1932; -   
KW Complete proteome; Hypothetical protein.   
SQ SEQUENCE 35 AA; 4255 MW; BD6B6261EC021297 CRC64;

Query Match 15.3%; Score 41; DB 2; Length 35;   
Best Local Similarity 40.7%; Pred. No. 6.8e+02;   
Matches 11; Conservative 2; Mismatches 8; Indels 6; Gaps 1;

Qy 12 LYKGDPAKY-----KNPERWYRASF 32   
| | | | | | | | | | | | | | | | | | | | | |   
Db 3 LYKGTPLSLVFLSYLKLREGYRDTF 29

RESULT 5   
ID Q7R533 PRELIMINARY; PRT; 42 AA.   
AC Q7R533;   
DT 01-MAR-2004 (TREMELrel. 26, Created)   
DT 01-MAR-2004 (TREMELrel. 26, Last sequence update)   
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)   
DE GLP\_137\_14369\_14497.   
OS Giardia lamblia ATCC 50803.   
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.   
OX NCBI\_TaxID=184922;   
RN [1]   
RP SEQUENCE FROM N.A.   
RC STRAIN-WB C6;   
RA Morrison H.G.;   
RA Olsen G.J.; Sogin M.L.;   
RA "Draft sequence of the Giardia lamblia genome.";   
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.   
CC -!- CAUTION: The sequence shown here is derived from an   
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is   
CC preliminary data.   
DR EMBL; AACB01000007; EAA42371.1; -   
SQ SEQUENCE 42 AA; 5099 MW; PE54073628B9D8A7 CRC64;

Query Match 15.3%; Score 41; DB 2; Length 42;   
Best Local Similarity 24.0%; Pred. No. 8.2e+02;   
Matches 6; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

Qy -14 KEGDPAPYKNPERWYRASPPIITVT 38   
| | | | | | | | | | | | | | | | | | | | | |   
Db 8 KRRSKPLATPCCKWQSPHPLSL 32

RESULT 6   
ID Q70U90 PRELIMINARY; PRT; 47 AA.   
AC Q70U90;   
DT 05-JUL-2004 (TREMELrel. 27, Created)   
DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)   
DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)   
DE Laccase (EC 1.10.3.2) (Fragment).   
GN Name=lac;   
OS Mycena pura.   
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;   
OC Agaricales; Tricholomataceae; Mycena.   
OX NCBI\_TaxID=153505;   
RN [1]   
RP SEQUENCE FROM N.A.   
RA Luis P.; Walther G.; Martin F.; Buscot F.;   
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.   
DR EMBL; AJ542630; CAD65822.1; -   
DR HSSP; Q9Y780; 1A65.   
DR GO; GO:0008471; F.laccase activity; IEA.   
DR GO; GO:0016491; F:oxidoreductase activity; IEA.   
DR InterPro; IPR008972; Cupredoxin.

KW Oxidoreductase.   
FT NON\_TER 1   
FT NON\_TER 47   
SQ SEQUENCE 47 AA; 5404 MW; A6437ERFD6D9A8C4 CRC64;

Query Match 15.3%; Score 41; DB 2; Length 47;   
Best Local Similarity 34.8%; Pred. No. 9.3e+02;   
Matches 16; Conservative 4; Mismatches 16; Indels 10; Gaps 3;

Qy 5 YGDFQFALYKEGDPAPYKN-----PERWYRASPPIITVTAAHSGTY 45   
: | | | | | | | | | | | | | | | | | | | | | |   
Db 3 HGFFQFKTASEDGA-FVNQCPIAPNTTYISFS-----TANQTGTF 43

RESULT 7   
ID Q8NFW3 PRELIMINARY; PRT; 20 AA.   
AC Q8NFW3;   
DT 01-OCT-2002 (TREMELrel. 22, Created)   
DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)   
DT 01-OCT-2002 (TREMELrel. 22, Last annotation update)   
DE Synovial sarcoma SY7/SSX1 fusion protein (Fragment).   
GN Name=SY7/SSX1 fusion;   
OS Homo sapiens (Human).   
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;   
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.   
OX NCBI\_TaxID=9606;   
RN [1]   
RP SEQUENCE FROM N.A.   
RA Tamborini E.; Agus V.; Pierotti M.A.; Pilotti S.; Rosai J.;   
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.   
DR EMBL; AF402619; AAM95901.1; -   
FT NON\_TER 1   
FT NON\_TER 20   
SQ SEQUENCE 20 AA; 2377 MW; F1534C73F9108883 CRC64;

Query Match 14.6%; Score 39; DB 2; Length 20;   
Best Local Similarity 46.7%; Pred. No. 6.7e+02;   
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 2 QTRYGFDQFALYKEG 16   
| | | | | | | | | | | | | | | |   
Db 2 QRPYGYDQFGPQNDG 16

RESULT 8   
ID Q8UUN6 PRELIMINARY; PRT; 32 AA.   
AC Q8UUN6;   
DT 01-MAR-2002 (TREMELrel. 20, Created)   
DT 01-MAR-2002 (TREMELrel. 20, Last sequence update)   
DT 01-MAR-2002 (TREMELrel. 20, Last annotation update)   
DE Beta-TrCP protein (Fragment).   
GN Name=beta-TrCP;   
OS Xenopus laevis (African clawed frog).   
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;   
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;   
OC Xenopodinae; Xenopus.   
OX NCBI\_TaxID=8355;   
RN [1]   
RP SEQUENCE FROM N.A.   
RA Ballarino M.;   
RT "Analisi strutturale e funzionale del gene beta-TrCP in Xenopus   
RT laevis.";   
RL Thesis (2001), Department of Genetics and Molecular Biology "Charles   
RL Darwin", University of Rome La Sapienza, Rome, Italy.   
RN [2]   
RP SEQUENCE FROM N.A.   
RA Carnevali F.;   
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.   
DR EMBL; AJ428935; CAD21932.1; -   
FT NON\_TER 1   
FT NON\_TER 32

SQ SEQUENCE 32 AA; 3739 MW; E26431D00A780CFB CRC64;  
 Query Match 14.6%; Score 39; DB 2; Length 32;  
 Best Local Similarity 37.5%; Pred. No. 1.1e+03;  
 Matches 9; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

QY 12 LYKEGDPAPYKNPWRWTRASFPII 35  
 :|||:||||:||||:  
 DB 4 LFNKPKPDGKTPPNSFYRALYPKI 27

RESULT 9  
 O24624 PRELIMINARY; PRT; 33 AA.  
 ID O24624  
 AC O24624;  
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
 DT 05-JUN-2004 (TrEMBLrel. 27, Last annotation update)  
 DE NADPH:protochlorophyllide oxidoreductase porB (Fragment).  
 GN Name=porB-II; Synonyms=porB-I;  
 OS Pinus taeda (Loblolly pine).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.  
 OC NCBI\_taxid=3352;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Cotyledon;  
 RX MEDLINE=99003724; PubMed=9787456;  
 RA Skinner J.S., Timko M.P.;  
 RT "Loblolly pine (Pinus taeda L.) contains multiple expressed genes  
 RT encoding light-dependent NADPH:protochlorophyllide oxidoreductase  
 RT (POR).";  
 RL Plant Cell Physiol. 39:795-806(1998).  
 DR EMBL; AF027347; AAB86725.1; -  
 DR EMBL; AF027342; AAB86720.1; -  
 DR GO; GO:0003700; F:transcription factor activity; IEA.  
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro; IPR002197; HTH\_Fis.  
 DR PRINTS; PR01590; HTHFIS.  
 DR NON TER 33  
 FT 33  
 SQ SEQUENCE 33 AA; 3303 MW; 4B781255B3EB6AFB CRC64;  
 Query Match 14.6%; Score 39; DB 2; Length 33;  
 Best Local Similarity 60.0%; Pred. No. 1.1e+03;  
 Matches 9; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 QTRYGFPQFALYKEG 16  
 |||:|||||  
 DB 6 QTHIGSAAFALQKEG 20

RESULT 10  
 Q9HF16 PRELIMINARY; PRT; 39 AA.  
 ID Q9HF16  
 AC Q9HF16;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Actin (Fragment).  
 GN Name=actl;  
 OS Epichloe amazillans.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Hypocreomycetidae; Hypocreales; Clavicipitaceae; Epichloe.  
 OC NCBI\_taxid=42805;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC200744;  
 RA Craven K.D., Hsiau P.T.W., Leuchmann A., Hollin W., Scharld C.L.;  
 RT "Multigene phylogeny of Epichloe species, fungal symbionts of  
 RT grasses.";  
 RL Ann. Mo. Bot. Gard. 88:14-34 (2001).  
 DR EMBL; AF240083; AAG39691.1; -  
 DR GO; GO:0015629; C:actin cytoskeleton; IEA.

```
RL SvDowia 54:98-117(2002).
DR EMBL; AF368348; AM20836.2; -.
FT NON TER 1
SQ SEQUENCE 41 AA; 4579 MW; 4409FA444FD8C985 CRC64;

Query Match 14.6%; Score 39; DB 2; Length 41;
Best Local Similarity 28.6%; Pred. No. 1.5e+03;
Matches 6; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 20 PYKNPERWYRASFPITVTAA 40
DB 17 PPSDFWHRTFLPTSS 37

RESULT 13
Q80B18 PRELIMINARY; PRT; 46 AA.
AC Q80B18;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein (Fragment).
OS Saimiriine herpesvirus 2.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Rhadinovirus.
OX NCBI_TaxID=10381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B6045;
RX MEDLINE=22918177; PubMed=14554077; DOI=10.1016/S0042-6822(03)00449-5;
RA Ensser A., Thureau M., Wittmann S., Fickenscher H.;
RT "The genome of herpesvirus saimiri C488 which is capable of
transforming human T cells.";
RL Virology 314:471-487(2003).
DR EMBL; AJ410485; CAC85013.1; -.
KW Hypothetical protein.
FT NON TER 46
SQ SEQUENCE 46 AA; 5325 MW; C5EDBFA59871761E CRC64;

Query Match 14.6%; Score 39; DB 2; Length 46;
Best Local Similarity 70.0%; Pred. No. 1.6e+03;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 20 PYKNPERWYR 29
DB 2 PYKVPPIYYR 11

RESULT 14
Q80BJ4 PRELIMINARY; PRT; 46 AA.
AC Q80BJ4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein (Fragment).
OS Saimiriine herpesvirus 2.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Rhadinovirus.
OX NCBI_TaxID=10381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A6051;
RX MEDLINE=22918177; PubMed=14554077; DOI=10.1016/S0042-6822(03)00449-5;
RA Ensser A., Thureau M., Wittmann S., Fickenscher H.;
RT "The genome of herpesvirus saimiri C488 which is capable of
transforming human T cells.";
RL Virology 314:471-487(2003).
DR EMBL; AJ410483; CAC85007.1; -.
KW Hypothetical protein.
FT NON TER 46
SQ SEQUENCE 46 AA; 5325 MW; C5EDBFA59871761E CRC64;
```

```
Query Match 14.6%; Score 39; DB 2; Length 46;
Best Local Similarity 70.0%; Pred. No. 1.6e+03;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 20 PYKNPERWYR 29
DB 2 PYKVPPIYYR 11

RESULT 15
Q80BJ7 PRELIMINARY; PRT; 46 AA.
AC Q80BJ7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein (Fragment).
OS Saimiriine herpesvirus 2.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Rhadinovirus.
OX NCBI_TaxID=10381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A5747;
RX MEDLINE=22918177; PubMed=14554077; DOI=10.1016/S0042-6822(03)00449-5;
RA Ensser A., Thureau M., Wittmann S., Fickenscher H.;
RT "The genome of herpesvirus saimiri C488 which is capable of
transforming human T cells.";
RL Virology 314:471-487(2003).
DR EMBL; AJ410482; CAC85001.1; -.
KW Hypothetical protein.
FT NON TER 46
SQ SEQUENCE 46 AA; 5325 MW; C5EDBFA59871761E CRC64;

Query Match 14.6%; Score 39; DB 2; Length 46;
Best Local Similarity 70.0%; Pred. No. 1.6e+03;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 20 PYKNPERWYR 29
DB 2 PYKVPPIYYR 11

RESULT 16
Q80BR5 PRELIMINARY; PRT; 46 AA.
AC Q80BR5;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein (Fragment).
OS Saimiriine herpesvirus 2.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Rhadinovirus.
OX NCBI_TaxID=10381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A6355;
RX MEDLINE=22918177; PubMed=14554077; DOI=10.1016/S0042-6822(03)00449-5;
RA Ensser A., Thureau M., Wittmann S., Fickenscher H.;
RT "The genome of herpesvirus saimiri C488 which is capable of
transforming human T cells.";
RL Virology 314:471-487(2003).
DR EMBL; AJ410484; CAC84287.1; -.
KW Hypothetical protein.
FT NON TER 46
SQ SEQUENCE 46 AA; 5325 MW; C5EDBFA59871761E CRC64;

Query Match 14.6%; Score 39; DB 2; Length 46;
Best Local Similarity 70.0%; Pred. No. 1.6e+03;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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Qy      20 PYKNPERWYR 29
      |||||:|
Db      2 PYKVPEIYYR 11

RESULT 17
Q6V8T8 PRELIMINARY; PRT; 47 AA.
ID Q6V8T8
AC Q6V8T8; 205-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Methylcochlorine hydroxylase (Fragment)
OS Malus domestica (Apple) (Malus sylvestris)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Rosales; Rosaceae; Maloideae; Malus.
OX NCBI_TaxID=3750;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RA Venise J.-S., Pontais I., Paulin J.-P., Brisset M.-N.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the cytochrome P450 family.
DR EMBL: AY347798; AAQ54507.1; -
DR GO: 0004497; F:monooxygenase activity; IEA.
DR GO: 0006118; P:electron transport; IEA.
DR InterPro: IPR011128; Cytochrome_P450.
DR InterPro: IPR002403; EP450IV.
DR Pfam: PF00067; P450; 1.
DR PRINTS: PR00465; EP450IV.
KW Heme.
FT NON_TER 1
FT NON_TER 47
FT NON_TER 47
SQ SEQUENCE 47 AA; 5453 MW; 14E4263B242E9133 CRC64;

Query Match 14.6%; Score 39; DB 2; Length 47;
Best Local Similarity 54.5%; Pred. No. 1.7e+03;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      17 DPAPYKNPERW 27
      |||||:|
Db      7 DPETYENPEY 17

RESULT 18
Q6U847 PRELIMINARY; PRT; 40 AA.
ID Q6U847
AC Q6U847; 205-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Methyltransferase C (Fragment).
GN Name=mtfC;
OS Mycobacterium intracellulare.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1767;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=5509-Borstel;
RA Krzywinska E., Krzywinski J., Schorey J.S.;
RL "Phylogeny of Mycobacterium avium strains inferred from
RT glycopeptidolipid biosynthesis pathway genes.";
RL Microbiology 0:0-0(2004).
DR EMBL: AY376382; AAR24910.1; -
DR GO: 0008168; F:methyltransferase activity; IEA.
DR GO: 0016740; F:transferase activity; IEA.
KW Methyltransferase; Transferase.
FT NON_TER 40
FT NON_TER 40
FT NON_TER 40
SQ SEQUENCE 40 AA; 4729 MW; 2435FB1DE46F0767 CRC64;

Query Match 14.4%; Score 38.5; DB 2; Length 40;

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Best Local Similarity 47.4%; Pred. No. 1.6e+03;
Matches 9; Conservative 2; Mismatches 5; Indels 3; Gaps 1;

Qy      3 TRYGFDOF---ALYKEGDP 18
      |||||:|
Db      19 TRYGSDELVPVGLYRLGRP 37

RESULT 19
Q7GI10 PRELIMINARY; PRT; 28 AA.
ID Q7GI10
AC Q7GI10; 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE NADPH:protochlorophyllide oxidoreductase porB (Fragment).
GN Names=porB-II;
OS Pinus taeda (Loblolly pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=3352;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cotyledon;
RX MEDLINE=99003724; PubMed=9787456;
RA Skinner J.S., Timko M.P.;
RL "Loblolly pine (Pinus taeda L.) contains multiple expressed genes
RT encoding light-dependent NADPH:protochlorophyllide oxidoreductase
RT (POR).";
RL Plant Cell Physiol. 39:795-806(1998).
DR EMBL: AF027346; AAB86724.1; -
FT NON_TER 28
FT NON_TER 28
FT NON_TER 28
SQ SEQUENCE 28 AA; 2855 MW; 13DDAB3AA1EF0E69 CRC64;

Query Match 14.2%; Score 38; DB 2; Length 28;
Best Local Similarity 60.0%; Pred. No. 1.3e+03;
Matches 9; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      2 QTRYGFDOFALYKEG 16
      |||||:|
Db      6 QTHIGSVAFALQKEG 20

RESULT 20
Q96WI2 PRELIMINARY; PRT; 32 AA.
ID Q96WI2
AC Q96WI2; 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Actin (Fragment).
OS Neotrophodum siegelii.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Clavicipitaceae;
OC mitosporic Clavicipitaceae; Neotyphodium.
OX NCBI_TaxID=163304;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 74483;
RA Craven K.D., Blankenship J.D., Leuchtmann A., Hignight K.,
RA Schardl C.L.;
RL "Hybrid fungal endophytes symbiotic with the grass Lolium pratense.";
RL Sydowia 53:44-73(2001).
DR EMBL: AF308137; AAK70932.1; -
DR GO: 0015629; C:actin cytoskeleton; IEA.
DR GO: 0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro: IPR004000; Actin_like.
DR Pfam: PF00022; Actin; 1.
FT NON_TER 1
FT NON_TER 32
FT NON_TER 32
SQ SEQUENCE 32 AA; 3272 MW; 003FBD545FCE13A5 CRC64;

Query Match 14.3%; Score 38; DB 2; Length 32;

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Best Local Similarity 39.3%; Pred. No. 1.5e+03;  
Matches 11; Conservative 0; Mismatches 9; Indels 8; Gaps 1;

Qy 16 GDPAKYKNPERWYRASFPFIITVTAHSG 43  
Db 13 GDDAP-----RAVFPISVGRPRHQ 32

RESULT 21

ID Q24637 PRELIMINARY; PRT; 33 AA.  
AC O24637;  
DT 01-JAN-1998 (TREMBlrel. 05, Created)  
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)  
DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE NADPH:protochlorophyllide oxidoreductase porB (Fragment).  
GN Name=porB-II; Synonym=porB-I;  
OS Pinus taeda (loblolly pine).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.  
OX NCBI\_TaxID=3352;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Cotyledon;  
RX MEDLINE=95003724; PubMed=9787456;  
RA Skinner J.S., Tinko M.P.;  
RT "Loblolly pine (Pinus taeda L.) contains multiple expressed genes  
RT encoding light-dependent NADPH:protochlorophyllide oxidoreductase  
RT (POR).";  
RL Plant Cell Physiol. 39:795-806(1998).  
DR EMBL; AF027345; AAB86723.1; -  
DR EMBL; AF027338; AAB86716.1; -  
DR EMBL; AF027339; AAB86717.1; -  
DR EMBL; AF027340; AAB86718.1; -  
DR EMBL; AF027341; AAB86719.1; -  
DR EMBL; AF027343; AAB86721.1; -  
DR EMBL; AF027344; AAB86722.1; -  
DR GO; GO:0003700; F:transcription factor activity; IEA.  
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR InterPro; IPR002197; HTH\_Fis.  
DR PRINTS; PR01590; HTHFIS.  
FT NON TER 33  
SQ SEQUENCE 33 AA; 3331 MW; 48781255B3F3DDAB CRC64;

Query Match 14.2%; Score 38; DB 2; Length 33;  
Best Local Similarity 60.0%; Pred. No. 1.5e+03;  
Matches 9; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 QTRYGFDQFALYKEG 16  
Db 6 QTHIGSVAFALQKEG 20

RESULT 22

ID Q7LTM6 PRELIMINARY; PRT; 39 AA.  
AC Q7LTM6;  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE Actin (Fragment).  
GN Name=act1;  
OS Epichloe typhina.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
OC Hypocreomycetidae; Hypocreales; Clavicipitaceae; Epichloe.  
OX NCBI\_TaxID=5113;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC201667;  
RA Craven K.D., Hsiau P.T.W., Leuchtmann A., Hollin W., Schardl C.L.;  
RT "Multigene phylogeny of Epichloe species, fungal symbionts of  
RT grasses.";  
RL Ann. Mo. Bot. Gard. 88:14-34(2001).

DR EMBL; AF240114; AAG39722.1; -  
FT NON TER 1  
FT NON TER 39  
SQ SEQUENCE 39 AA; 3967 MW; 2C7E3265EA20F58C CRC64;

Query Match 14.2%; Score 38; DB 2; Length 39;  
Best Local Similarity 39.3%; Pred. No. 1.9e+03;  
Matches 11; Conservative 0; Mismatches 9; Indels 8; Gaps 1;

Qy 16 GDPAKYKNPERWYRASFPFIITVTAHSG 43  
Db 20 GDDAP-----RAVFPISVGRPRHQ 39

RESULT 23

ID Q7LTM7 PRELIMINARY; PRT; 39 AA.  
AC Q7LTM7;  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE Actin (Fragment).  
GN Name=act1;  
OS Epichloe typhina.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
OC Hypocreomycetidae; Hypocreales; Clavicipitaceae; Epichloe.  
OX NCBI\_TaxID=5113;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC201666;  
RA Craven K.D., Hsiau P.T.W., Leuchtmann A., Hollin W., Schardl C.L.;  
RT "Multigene phylogeny of Epichloe species, fungal symbionts of  
RT grasses.";  
RL Ann. Mo. Bot. Gard. 88:14-34(2001).  
DR EMBL; AF240113; AAG39721.1; -  
FT NON TER 1  
FT NON TER 39  
SQ SEQUENCE 39 AA; 3967 MW; 2C7E3265EA20F58C CRC64;

Query Match 14.2%; Score 38; DB 2; Length 39;  
Best Local Similarity 39.3%; Pred. No. 1.9e+03;  
Matches 11; Conservative 0; Mismatches 9; Indels 8; Gaps 1;

Qy 16 GDPAKYKNPERWYRASFPFIITVTAHSG 43  
Db 20 GDDAP-----RAVFPISVGRPRHQ 39

RESULT 24

ID Q7LTM8 PRELIMINARY; PRT; 39 AA.  
AC Q7LTM8;  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE Actin (Fragment).  
GN Name=act1;  
OS Epichloe typhina.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
OC Hypocreomycetidae; Hypocreales; Clavicipitaceae; Epichloe.  
OX NCBI\_TaxID=5113;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=E348;  
RA Craven K.D., Hsiau P.T.W., Leuchtmann A., Hollin W., Schardl C.L.;  
RT "Multigene phylogeny of Epichloe species, fungal symbionts of  
RT grasses.";  
RL Ann. Mo. Bot. Gard. 88:14-34(2001).  
DR EMBL; AF240112; AAG39720.1; -  
FT NON TER 1  
FT NON TER 39  
SQ SEQUENCE 39 AA; 3967 MW; 2C7E3265EA20F58C CRC64;

Query Match 14.2%; Score 38; DB 2; Length 39;  
 Best Local Similarity 39.3%; Pred. No. 1.9e+03;  
 Matches 11; Conservative 0; Mismatches 9; Indels 8; Gaps 1;

Qy 16 GDPAPYKNPERWYRASFPFIITVTAHSG 43  
 |||||  
 Db 20 GDDAP-----RAVFPISIVGRPRHQG 39

RESULT 25

Q7LTM9 PRELIMINARY; PRT; 39 AA.  
 AC Q7LTM9;  
 DT 05-JUL-2004 (TREMBlrel. 27, Created)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
 DE Actin (Fragment).  
 GN Name=act1;  
 OS Epichloe typhina.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Hypocreomycetidae; Hypocreales; Clavicipitaceae; Epichloe.  
 OX NCBI\_TaxID=5113;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC200851;  
 RA Craven K.D., Hsiau P.T.W., Leuchtmann A., Hollin W., Schardl C.L.;  
 RT "Multigene phylogeny of Epichloe species, fungal symbionts of  
 RL grasses.";  
 RL Ann. Mo. Bot. Gard. 88:14-34 (2001).  
 DR EMBL; AF240111; AAG39719.1; -.  
 FT NON\_TER 1  
 FT NON\_TER 39  
 SQ SEQUENCE 39 AA; 3967 MW; 2C7E3265EA20F58C CRC64;

Query Match 14.2%; Score 38; DB 2; Length 39;  
 Best Local Similarity 39.3%; Pred. No. 1.9e+03;  
 Matches 11; Conservative 0; Mismatches 9; Indels 8; Gaps 1;

Qy 16 GDPAPYKNPERWYRASFPFIITVTAHSG 43  
 |||||  
 Db 20 GDDAP-----RAVFPISIVGRPRHQG 39

Search completed: October 29, 2005, 04:27:50  
 Job time : 178 secs